

Hart, Edward

89452

From: Ungar, Susan
Sent: Wednesday, March 19, 2003 3:30 PM
To: Hutzell, Paula
Cc: Hart, Edward
Subject: Rush Sequence Search for 09/674,975

Hi

I need a rush sequence search for 09/674,975, SEQ ID NOs 1 and 2. These are both peptides. Just realized that I need to get this case in this biweek.

Please forward this search to Ed Hart who has agreed to submit it for me.

Thanks

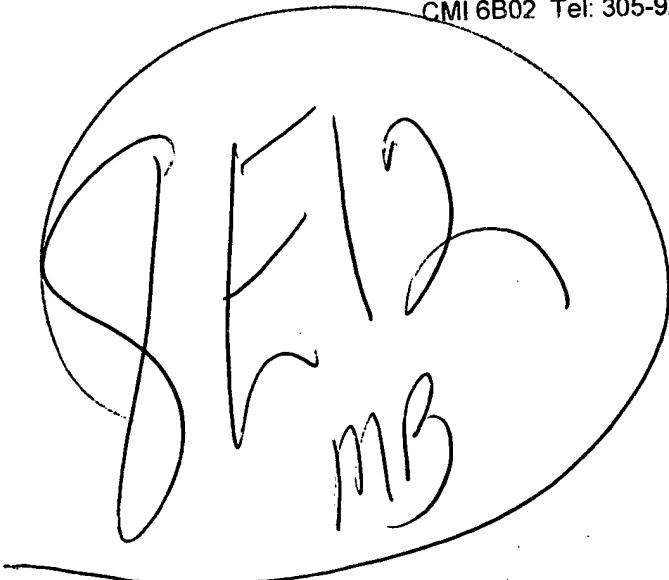
Susan Ungar

1642

103-305-2181

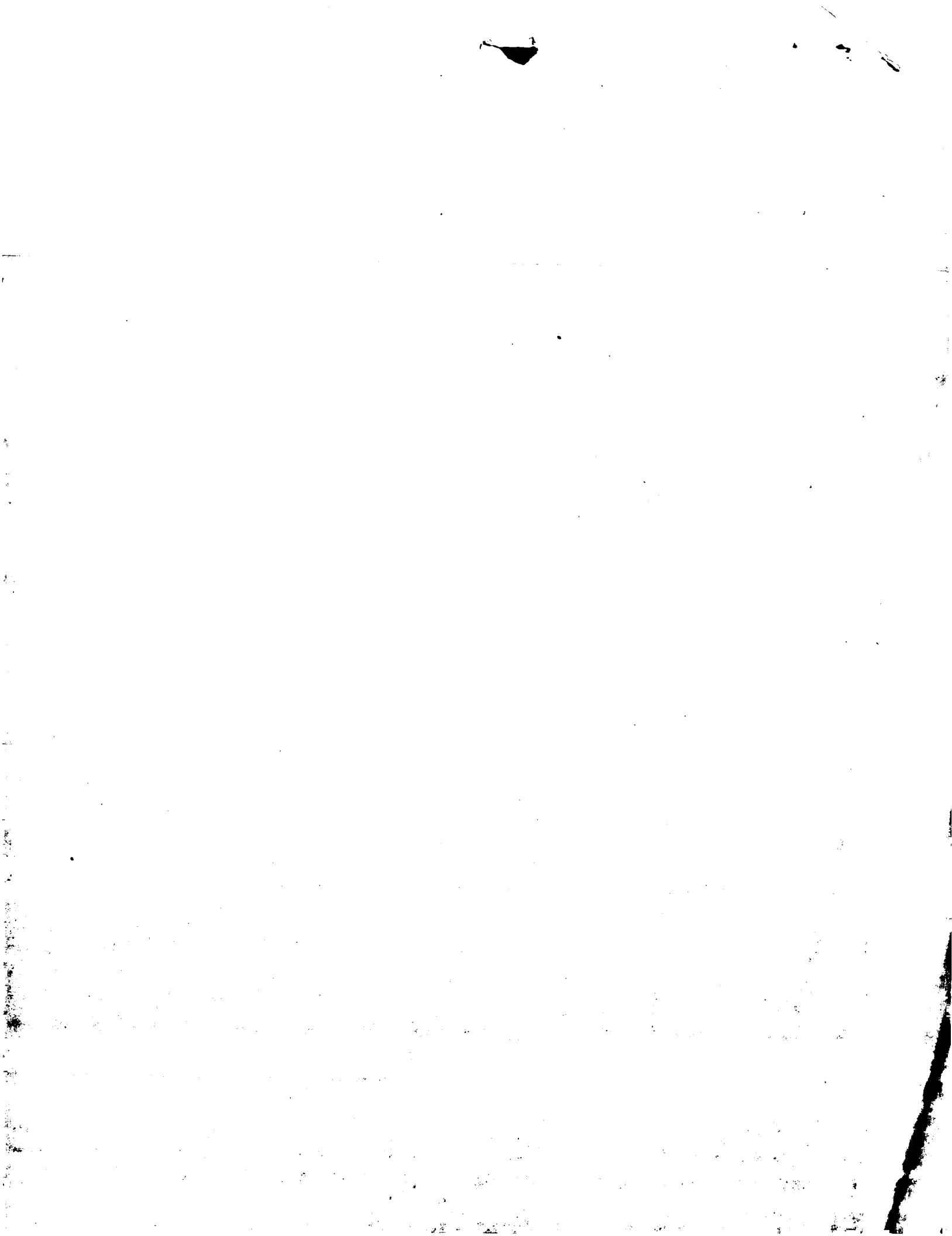
CMI-8B05

Edward Hart
Technicai Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203



3/19/03
Comparison 1P
2-ATA

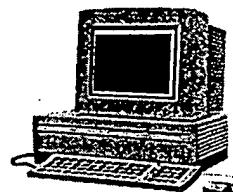
3/20/03
Completed



BioTech-Chem Library

Search Results

Feedback Form (Optional)



Scientific & Technical Information

The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact *the BioTech-searcher* who conducted the search *or contact:*

**Mary Hale, Supervisor, 308-
CM-1 Room 1E01**

Voluntary Results Feedback Form

➤ *I am an examiner in Workgroup:* (Example: 1610)

➤ *Relevant prior art found, search results used as follows:*

- 102 rejection
- 103 rejection
- Cited as being of interest.
- Helped examiner better understand the invention.
- Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- Foreign Patent(s)
- Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ *Relevant prior art not found:*

- Results verified the lack of relevant prior art (helped determine patentability).
- Search results were not useful in determining patentability or understanding the invention.

Other Comments:

Drop off completed forms at the Circulation Desk CM-1, or send to Mary Hale, CM1-1E01 or
mary.hale@uspto.gov



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OM protein - protein search, using sw model

Run on:

March 19, 2003, 17:18:13 ; Search time 32.5 Seconds

{without alignments} 180.401 Million cell updates/sec

Title: US-09-674-975-1

Perfect score: 243

Sequence: 1 KISHFLKMESELNFIRAHPTV..... NCEPANPSEKNSPSTQYCYS 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_101002:*

1: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1980.DAT:*

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6: /SIDS1/gcdata/geneseq/geneseq/geneseq-emb1/AA1987.DAT:*

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18: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2005.DAT:*

19: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2006.DAT:*

20: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2007.DAT:*

21: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2008.DAT:*

22: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2009.DAT:*

23: /SIDS1/gcdata/geneseq/geneseq-emb1/AA2010.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	243	100.0	44 21	AAY5000 Human CD20 protein
2	243	100.0	297 10	AAP21356 CD20.4 antigen.
3	243	100.0	297 13	AAR20808 Human CD20 antigen
4	243	100.0	297 17	AAR21436 Human CD20 antigen
5	243	100.0	297 19	AARW045 Human CD20.4 antigen
6	243	100.0	297 20	AARW6192 Human CD20.4 antigen
7	243	100.0	297 21	AYW6131 Human lymphocyte surface
8	243	100.0	297 22	AAU02440 Human lymphocyte c
9	212	87.2	150 22	AAMW0564 Human haematologic
10	212	87.2	150 22	AAMW0569 Human haematologic

RESULT 1		ALIGNMENTS	
ID	AYY5000	standard; peptide; 44 AA.	
XX			
AC	AYY5000;		
XX			
DT	18-FEB-2000 (first entry)		
XX			
DE	Human CD20 protein fragment.		
XX			
KW	CD20; active vaccination; autologous cell; transmembrane protein; cancer; B cell Non-Hodgkin's lymphoma; B cell disease; autoimmune disorder; chronic lymphocytic leukaemia; B-cell regulatory disorder; therapy; human.		
KW			
OS	Homo sapiens.		
XX			
PN	W0957981-A1.		
XX			
PD	18-NOV-1999.		
XX			
PF	07-MAY-1999; 99WO-US10065.		
XX			
PR	08-MAY-1998; 98US-0084870.		
XX			
PA	(SLOC) SLOAN KETTERING INST CANCER RES.		
XX			
PI	Agus DB, Scheinberg D, Roberts W, zelenetz AD;		
XX			
DR	WPI: 2000-038920/03.		
XX			
PT	Novel compositions and methods utilizing a humoral immune response to treat B cell Non-Hodgkin's lymphoma and other diseases -		

PI	Aruffo A,	Seed B;
XX		
XX	WPI; 1998-609251/51.	
DR	N-PSDB; AAV63448.	
PT	New cloning vector and polylinker - based on existing sequences for efficient cloning and expression of mammalian cDNA(s), especially human lymphocyte antigenic sequences	
XX		
PS	Example 6; Fig 10A-B; 79pp; English.	
XX		
CC	This polypeptide comprises human CD20.4 antigen. Its amino acid sequence was deduced from the nucleotide sequence (see AAV63448) of a cDNA clone isolated from a Daudi cell cDNA library using a novel method for cloning cDNAs from mammalian expression libraries. The method is based on transient expression of an antigen in eukaryotic cells and physical selection of cells expressing the antigen by adhesion to an antibody-coated substrate. It is useful for the isolation and cloning of any protein which can be expressed and transported to the cell surface membrane of a eukaryotic cell, and has been used to clone genes (see AAV63442-63) encoding cell surface antigens from mammalian lymphocytes (see AAV80440-55). CD20, a B-lymphocyte specific antigen (BL, Bp35), was expressed in COS cells as 2 protein species, CD20.4 and CD20.6. The purified genes and proteins are useful for immuno-diagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, diseases, and disorders of animals, including humans.	
XX		
CC	Sequence 297 AA;	
CC	Query Match 100.0%; Score 243; DB 19; Length 297; Best Local Similarity 100.0%; Pred. No. 2.9e-24; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CQ	
CC	1 KISHLKLMESLNFRIRAHPTYINYNCEPANPSEKNSPSTQCYCS 44	
CC	142 KISHFLKLMESLNFRIRAHPTYINYNCEPANPSEKNSPSTQCYCS 185	
SQ		
RESULT 6		
AW86192		
ID	AW86192 standard; Protein; 297 AA..	
XX		
AC	AAW86192;	
XX		
DT	10-MAY-1999 (first entry)	
DE	Human CD20.4 antigen.	
XX		
KW	CD20.4; cell surface antigen; human; cDNA library; B lymphocyte.	
XX		
OS	Homo sapiens.	
XX		
FH	Key Modified-site	Location/Qualifiers
FT	9.11	
FT	/note= "Asn is N-glycosylated"	
FT	51..103	
FT	/note= "hydrophobic region"	
FT	117..141	
FT	/note= "hydrophobic region"	
FT	183..203	
FT	/note= "hydrophobic region"	
FT	293..295	
FT	/note= "Asn is N-glycosylated"	
XX		
PN	USS849898-A.	
XX		
PD	15-DEC-1998.	
XX		
PF	07-JUN-1995; 950S-048547.	
XX		
PR	01-DEC-1992; 92US-0983647.	
XX		
PR	25-FEB-1998; 88US-0160416.	
PR	13-JUL-1998; 89US-0379076.	
PR	23-MAR-1990; 90US-0498809.	
PR	13-JUL-1990; 90US-0553759.	
PR	07-JUN-1995; 95US-0485447.	
PA	(GEHO) GEN HOSPITAL CORP.	
XX		
DR	N-PSDB; AAV81206.	
XX		
PS	Example 6; Fig 10A-B; 79pp; English.	
XX		
CC	This polypeptide comprises human CD40 antigen - useful for cloning cDNA encoding cell surface antigens, constructing cDNA libraries, expression vectors for expression in eukaryotic cells or their fragments	
XX		
CC	Sequence 297 AA;	
CC	Query Match 100.0%; Score 243; DB 20; Length 297; Best Local Similarity 100.0%; Pred. No. 2.9e-24; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0; CQ	
CC	1 KISHLKLMESLNFRIRAHPTYINYNCEPANPSEKNSPSTQCYCS 44	
CC	142 KISHFLKLMESLNFRIRAHPTYINYNCEPANPSEKNSPSTQCYCS 185	
SQ		
RESULT 7		
AAV96131		
ID	AAV96131 standard; Protein; 297 AA..	
XX		
AC	AAV96131;	
XX		
DT	19-DEC-2000 (first entry)	
DE	Human cell surface antigen CD20.4.	
XX		
KW	CD20.4; cell surface antigen; human; immunoselection; panning; KW immunodiagnosis; diagnosis; immunotherapy; gene therapy; KW immune disorder; infection; asthma; immune-complex disease; KW amyloidosis; multiple sclerosis; parasitic disease..	
XX		
OS	Homo sapiens.	
XX		
FH	Key Region	Location/Qualifiers
FT	51..103	
FT	/note= "hydrophobic region"	
FT	117..141	
FT	/note= "hydrophobic region"	
FT	183..203	
FT	/note= "hydrophobic region"	

FT	Modified-site	9	OS	Homo sapiens.
FT	/note= "N-glycosylated"	293	PH	Key
FT	/note= "N-glycosylated"		FT	Location/Qualifiers
FT			FT	9..11
FT			FT	/note= "Asn is glycosylated"
FT			FT	51..103
FT			FT	/note= "Hydrophobic region"
FT			FT	117..141
FT			FT	/note= "Hydrophobic region"
FT			FT	183..203
FT			FT	/note= "Hydrophobic region"
FT			FT	293..295
FT			FT	/note= "Asn is glycosylated"
PD	29-AUG-2000.	XX	XX	
XX	28-OCT-1998;	98US-0181612.	XX	
XX	01-DEC-1992;	92US-0983647.	XX	
PR	25-FEB-1988;	88US-0160416.	XX	
PR	13-JUL-1989;	89US-0379076.	XX	
PR	23-MAR-1990;	90US-0498809.	XX	
PR	13-JUL-1990;	90US-0553759.	XX	
PA	(GEHO) GEN HOSPITAL CORP.	XX	XX	
PI	Stamenkovic I, Seed B;	XX	XX	
XX	WPI; 2000-586382/55.	XX	XX	
DR	N-PSDB; AAA50584.	XX	XX	
XX	Isolated nucleic acid molecule encoding the CD19 cell surface antigen, useful for immunodiagnosis and immunotherapy of immune-mediated diseases.	XX	XX	
PT	useful for immunodiagnosis and immunotherapy of immune-mediated diseases.	XX	XX	
PT	useful for immunodiagnosis and immunotherapy of immune-mediated diseases.	XX	XX	
PT	useful for immunodiagnosis and immunotherapy of immune-mediated diseases.	XX	XX	
PT	useful for immunodiagnosis and immunotherapy of immune-mediated diseases.	XX	XX	
PS	Example 6; Fig 10A-B; 75pp; English.	XX	XX	
XX	The present sequence is that of human cell surface antigen (CSA) CD20, as predicted from cDNA isolated from human Burkitt cell line Daudi cell library. CD20, (or B1, Bp35) is a pan B-cell antigen that plays an important role in B cell activation. The cDNA (see AA50584) was identified using a new method for cloning cDNAs encoding CSAs. The method is based upon transient expression of CSA in eukaryotic cells and physical selection of cells expressing CSA by adhesion to (panning on) an antibody-coated substrate such as a culture dish. CSA nucleic acids isolated by the method of the invention, and the proteins they encode, are useful for immunodiagnostic and immunotherapeutic applications, including the diagnosis and treatment of immune-mediated infections, and disorders in animals, including humans. These disorders include asthma, immune-complex disease, amyloidosis, parasitic diseases or multiple sclerosis.	XX	XX	
SQ	Sequence 297 AA;	XX	XX	
Query Match	100.0%; Score 243; DB 21; Length 297;	XX	XX	
Best Local Similarity	100.0%; Pred. No. 2.9e-24;	XX	XX	
Matches	44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	
OY	1 KISHLKLMESLNTRAHPTPYINIVCEANPSEKNSPSTQCY 44	XX	XX	
OY	1 KISHLKLMESLNTRAHPTPYINIVCEANPSEKNSPSTQCY 44	XX	XX	
Db	142 KISHLKLMESLNTRAHPTPYINIVCEANPSEKNSPSTQCY 185	XX	XX	
RESULT 8		XX	XX	
AAU02440	AAU02440 standard; Protein: 297 AA.	XX	XX	
ID		XX	XX	
AC	AAU02440;	XX	XX	
XX	29-AUG-2001 (first entry)	XX	XX	
DE	Human lymphocyte cell surface antigen CD20 Polypeptide.	XX	XX	
KW	Human; lymphocyte cell surface antigen; immune-mediated disease; CD20; infection; immune deficiency disorder; hypersensitivity; inflammation; systemic lupus erythematosus; platelet disorder; rheumatoid arthritis; transplant rejection; asthma.	XX	XX	
KW		XX	XX	
KW		XX	XX	
KW		XX	XX	
KW		XX	XX	
XX		XX	XX	
Query Match	100.0%; Score 243; DB 22; Length 297;	XX	XX	
Best Local Similarity	100.0%; Pred. No. 2.9e-24;	XX	XX	
Matches	44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX	XX	
OY	1 KISHLKLMESLNTRAHPTPYINIVCEANPSEKNSPSTQCY 44	XX	XX	
Db	142 KISHLKLMESLNTRAHPTPYINIVCEANPSEKNSPSTQCY 185	XX	XX	
RESULT 9		XX	XX	
ID	AAU02440 standard; Protein: 150 AA.	XX	XX	
AAU02440		XX	XX	

AC	AAM0564;	DE	13-NOV-2001 (first entry)
XX		XX	Human haematological malignancy-related antigen #267.
DT		XX	Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
XX		KW	Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
AC		KW	Homo sapiens.
XX		OS	Homo sapiens.
OS		XX	W0200164886-A2.
PN		XX	
XX		XX	07-SEP-2001.
PD		XX	
XX		XX	01-MAR-2001; 2001WO-US07272.
PF		XX	
XX		XX	01-MAR-2000; 2000US-0186126.
PR		XX	17-MAR-2000; 2000US-0190479.
PR		XX	27-APR-2000; 2000US-020545.
PR		XX	28-APR-2000; 2000US-0200303.
PR		XX	28-APR-2000; 2000US-020779.
PR		XX	01-MAY-2000; 2000US-0200999.
PR		XX	04-MAY-2000; 2000US-0202084.
PR		XX	04-MAY-2000; 2000US-0206201.
PR		XX	14-JUL-2000; 2000US-0218950.
PR		XX	03-AUG-2000; 2000US-0222003.
PR		XX	04-AUG-2000; 2000US-0222416.
PR		XX	07-AUG-2000; 2000US-0223378.
PR		XX	(CORI-) CORIXA CORP.
PA		XX	
XX		XX	Gaiger A, Algata PA, Mannion J;
PA		XX	
XX		XX	WPI; 2001-514842/56.
PT		XX	
PT		XX	Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukaemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma -
PT		XX	PS
PT		XX	Claim 1; Page 617; 1252pp; English.
XX		XX	
CC		XX	The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The
CC		XX	present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma.
CC		XX	SQ
CC		XX	Sequence 150 AA;
CC		XX	Query Match 87.2%; Score 212; DB 22; Length 150;
CC		XX	Best Local Similarity 100.0%; Pred. No. 1.8e-20; Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC		XX	QY 7 KMESLNFIKRAHTPYINYINCEPANPSEKNSPSTQCY 44
CC		XX	Db 1 KMESLNFIKRAHTPYINYINCEPANPSEKNSPSTQCY 38
CC		XX	RESULT 11
CC		XX	AAM0610
CC		XX	AAM0610 standard; Protein: 150 AA.
XX		XX	RESULT 10
XX		XX	AAM0569
XX		XX	AAM0569 standard; Protein: 150 AA.
AC		XX	AAM0569;
XX		XX	AAM0569;
DE		DE	Human haematological malignancy-related antigen #308.

XX Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX Homo sapiens.
 XX WO200164886-A2.
 XX 07-SEP-2001.
 PD 07-SEP-2001.
 XX 01-MAR-2001; 2001WO-US07272.
 PR 01-MAR-2000; 2000US-0186126.
 PR 17-MAR-2000; 2000US-0190479.
 PR 27-APR-2000; 2000US-0200545.
 PR 28-APR-2000; 2000US-0200303.
 PR 28-APR-2000; 2000US-0200779.
 PR 01-MAY-2000; 2000US-0200999.
 PR 01-MAY-2000; 2000US-0202084.
 PR 22-MAY-2000; 2000US-0206201.
 PR 14-JUL-2000; 2000US-0218950.
 PR 03-AUG-2000; 2000US-0222903.
 PR 04-AUG-2000; 2000US-0223416.
 PR 07-AUG-2000; 2000US-0223378.
 PR 07-AUG-2000; 2000US-0223378.
 XX PA (CORI-) CORIXA CORP.
 XX PI Gaiger A, Algata PA, Mannion J;
 XX DR WPI; 2001-514842/56.
 XX PT Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma -
 XX PS Claim 1; Pages 637-638; 1252pp; English.
 XX The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma.
 XX SQ Sequence 150 AA;
 XX Query Match 87.2%; Score 212; DB 22; Length 150;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-20;
 XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KMESLNFRAHPTPYINIYCEPANPSEKNSPSTQYCYS 44
 Db 1 KMESLNFRAHPTPYINIYCEPANPSEKNSPSTQYCYS 38
 RESULT 12
 ID AAM80619 standard; Protein; 150 AA.
 XX AC AAM80619;
 XX DT 13-NOV-2001 (first entry)
 XX DE Human haematological malignancy-related antigen #317.
 XX Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW Homo sapiens.
 KW follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 XX Homo sapiens.
 XX WO200164886-A2.
 XX 07-SEP-2001.
 PR 01-MAR-2001; 2001WO-US07272.
 PR 01-MAR-2000; 2000US-0186126.
 PR 17-MAR-2000; 2000US-0190479.
 PR 27-APR-2000; 2000US-0200545.
 PR 28-APR-2000; 2000US-0200303.
 PR 01-MAY-2000; 2000US-0200779.
 PR 04-MAY-2000; 2000US-0202084.
 PR 22-MAY-2000; 2000US-0206201.
 PR 14-JUL-2000; 2000US-0218950.
 PR 03-AUG-2000; 2000US-0222903.
 PR 04-AUG-2000; 2000US-0223416.
 PR 07-AUG-2000; 2000US-0223378.
 XX PA (CORI-) CORIXA CORP.
 XX PI Gaiger A, Algata PA, Mannion J;
 XX DR WPI; 2001-514842/56.
 XX PT Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma -
 XX PS Claim 1; Page 642; 1252pp; English.
 XX The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma.
 XX SQ Sequence 150 AA;
 XX Query Match 87.2%; Score 212; DB 22; Length 150;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-20;
 XX Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 KMESLNFRAHPTPYINIYCEPANPSEKNSPSTQYCYS 44
 Db 1 KMESLNFRAHPTPYINIYCEPANPSEKNSPSTQYCYS 38
 RESULT 13
 ID AAM0950 standard; Protein; 150 AA.
 XX AC AAM0950;
 XX DT 13-NOV-2001 (first entry)
 XX DE Human haematological malignancy-related antigen #648.
 XX Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
 KW haematological malignancy; antigen; chronic lymphocytic leukaemia;
 KW Homo sapiens.

PN	WO200164886-A2.
XX	
PD	07-SEP-2001.
XX	
XX	01-MAR-2001; 2001WO-US07272.
PF	
PR	01-MAR-2000; 2000US-0186126.
PR	17-MAR-2000; 2000US-019479.
PR	27-APR-2000; 2000US-020545.
PR	28-APR-2000; 2000US-020303.
PR	01-MAY-2000; 2000US-0200939.
PR	04-MAY-2000; 2000US-0202034.
PR	22-MAY-2000; 2000US-0205201.
PR	14-JUL-2000; 2000US-0218950.
PR	03-AUG-2000; 2000US-0222903.
PR	04-AUG-2000; 2000US-0223116.
PR	07-AUG-2000; 2000US-0223378.
PA	
XX	(CORT-) CORIXA CORP.
PI	
XX	Gaiger A, Algate PA, Mannion J;
DR	
XX	WPI; 2001-514842/56.
PT	Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma -
PT	Claim 1; Pages 773-774; 1252pp; English.
PS	
XX	The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma.
SQ	Sequence 150 AA;
Query Match	87.2%; Score 212; DB 22; Length 150;
Best Local Similarity	100.0%; Pred. No. 1.8e-20;
Matches	38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	KMESLNFRAHTPYINTYCEPANPSEKNSPSTQYCS 44
Db	1 KMESLNFRAHTPYINTYCEPANPSEKNSPSTQYCS 38
RESULT 14	
AAM81576	
ID	AAM81576 standard; Protein; 150 AA.
AC	
AC	AAM81576;
XX	
DT	13-NOV-2001 (first entry)
XX	
DE	Human haematological malignancy-related antigen #1274.
XX	
KW	Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
KW	
OS	Homo sapiens.
XX	
OS	WO200164886-A2.
PN	
XX	07-SEP-2001.
PN	
XX	WO200164886-A2.
PD	07-SEP-2001.
XX	
PF	01-MAR-2001; 2001WO-US07272.
XX	
PR	01-MAR-2000; 2000US-0186126.
PR	17-MAR-2000; 2000US-019479.
PR	27-APR-2000; 2000US-0200545.
PR	28-APR-2000; 2000US-0200303.
PR	01-MAY-2000; 2000US-0200939.
PR	04-MAY-2000; 2000US-0202034.
PR	22-MAY-2000; 2000US-0205201.
PR	14-JUL-2000; 2000US-0218950.
PR	03-AUG-2000; 2000US-0222903.
PR	04-AUG-2000; 2000US-0223116.
PR	07-AUG-2000; 2000US-0223378.
PA	
XX	(CORT-) CORIXA CORP.
PI	
XX	Gaiger A, Algate PA, Mannion J;
DR	
XX	WPI; 2001-514842/56.
PT	Compositions and methods for the detection of hematological malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma -
PT	Claim 1; Pages 1019-1020; 1252pp; English.
PS	
XX	The present invention relates to compositions and methods for the detection, diagnosis and therapy of haematological malignancies. The present sequence is the protein sequence of a human haematological malignancy related antigen. The methods of the present invention comprise detecting the presence of haematological malignancy related antigen(s) in a sample obtained from the patient (an increased level of the polypeptide, compared to an unaffected individual, is indicative of an increased risk). Haematological malignancies which can be treated using the present invention are chronic lymphocytic leukaemia, lymphoma, follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B cell non-Hodgkin's lymphoma.
SQ	Sequence 150 AA;
Query Match	87.2%; Score 212; DB 22; Length 150;
Best Local Similarity	100.0%; Pred. No. 1.8e-20;
Matches	38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	KMESLNFRAHTPYINTYCEPANPSEKNSPSTQYCS 44
Db	1 KMESLNFRAHTPYINTYCEPANPSEKNSPSTQYCS 38
RESULT 15	
AAM80488	
ID	AAM80488 standard; Protein; 146 AA.
AC	
AC	AAM80488;
XX	
DT	13-Nov-2001 (first entry)
XX	
DE	Human haematological malignancy-related antigen #186.
XX	
KW	Human; cytostatic; vascular; gene therapy; vaccine; lymphoma; haematological malignancy; antigen; chronic lymphocytic leukaemia; follicular lymphoma; Hodgkin's lymphoma; non-Hodgkin's lymphoma.
KW	
OS	Homo sapiens.
XX	
OS	WO200164886-A2.
PN	
XX	07-SEP-2001.
PN	
XX	WO200164886-A2.

XX
 PR 01-MAR-2000; 20000S-0186126.
 PR 17-MAR-2000; 20000S-0190479.
 PR 27-APR-2000; 20000S-0200545.
 PR 28-APR-2000; 20000S-0200303.
 PR 28-APR-2000; 20000S-0200779.
 PR 01-MAY-2000; 20000S-0200999.
 PR 04-MAY-2000; 20000S-0202084.
 PR 22-MAY-2000; 20000S-0206201.
 PR 14-JUL-2000; 20000S-0218950.
 PR 03-AUG-2000; 20000S-0222903.
 PR 04-AUG-2000; 20000S-0223416.
 PR 07-AUG-2000; 20000S-0223378.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Gaiger A, Algata PA, Mannion J;
 XX
 DR WPI; 2001-514842/56.
 XX
 PT Compositions and methods for the detection of hematological
 PT malignancies, e.g. chronic lymphocytic leukemia, lymphoma, follicular
 PT lymphoma and Hodgkin's and T/B cell non-Hodgkin's lymphoma
 XX
 PS Claim 1; Pages 584-585; 1252pp; English.
 XX
 CC The present invention relates to compositions and methods for the
 CC detection, diagnosis and therapy of haematological malignancies. The
 CC present sequence is the protein sequence of a human haematological
 CC malignancy related antigen. The methods of the present invention comprise
 CC detecting the presence of haematological malignancy related antigen(s) in
 CC a sample obtained from the patient (an increased level of the
 CC polypeptide, compared to an unaffected individual, is indicative of an
 CC increased risk). Haematological malignancies which can be treated using
 CC the present invention are chronic lymphocytic leukaemia, Lymphoma,
 CC follicular lymphoma, Hodgkin's lymphoma, non-Hodgkin's lymphoma and T/B
 CC cell non-Hodgkin's lymphoma.
 XX
 SQ Sequence 146 AA:

=
 Query Match 80.7%; Score 196; DB 22; Length 146;
 Best Local Similarity 94.7%; Pred. No. 2.4e-18;
 Matches 36; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 7 KMESLNFRAHTPYINYINCEPANPSEKNPSP7QYCS 44
 Db 1 KMESLNFRAHTPYINYINCEPANPSEKNPSP7QYCS 38

Search completed: March 19, 2003, 17:19:54
 Job time : 45.5 secs



OM protein - protein search, using sw model

Run on: March 19, 2003, 17:22:55 ; Search time 12 Seconds

Perfect score: 243

Sequence: 1 KISHFLKMEISLNFIKHTPY..... NCEPANPSEKNSPSTQYCYS 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /con2_6/ptodata/2/1aa/5A_COMB.pep:*

2: /con2_6/ptodata/2/1aa/5B_COMB.pep:*

3: /con2_6/ptodata/2/1aa/6A_COMB.pep:*

4: /con2_6/ptodata/2/1aa/6B_COMB.pep:*

5: /con2_6/ptodata/2/1aa/PCUTS_COMB.pep:*

6: /con2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

US-09-446-855A-2

; Sequence 2, Application: US/08446855A

; Patent No. 584953

; GENERAL INFORMATION:

; APPLICANT: Stewart, Thomas S

; APPLICANT: Flores, Maria V

; APPLICANT: O'Sullivan, William J

; TITLE OF INVENTION: Nucleotide sequence encoding carbamoyl phosphate synthetase II

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESS: Nixon & Vanderhye PC

; STREET: 1100 No. 5849573th Glebe Road, 8th Floor

; CITY: Arlington

; STATE: Virginia

; COUNTRY: USA

ZIP: 22201-4714

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent-In Release #1.24

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08446.855A

FILING DATE: 06-Jul-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Mitchard, Leonard C

REGISTRATION NUMBER: 29.009

REFERENCE/DOCKET NUMBER: 47-80

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-816-4100

TELEFAX: 703-816-4100

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

SEQUENCE LENGTH: 2301 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-446-855A-2

Query match 24 %; Score 60.5; DB 2; Length 2391;

Best Local Similarity 34.3%; Pred. No. 12; Sequence 3, Appli

Matches 12; Conservative 10; Mismatches 12; Indels 1; Gaps 1;

Qy 2 ISHFLKMEISLNFIKHTPY-NIVCEPANPSEN 35

Db 317 INHTLDRKNLITSEEEVYLHNCNFSSNSDRN 351

28 47.5 19.5 437 2 US-08-481-814A-7

29 47.5 19.5 944 4 US-09-449-285A-2

30 47 19.3 1 1 US-08-360-3

31 47 19.3 126 2 US-08-888-497-38

32 47 19.3 126 4 US-09-362-230-38

33 47 19.3 126 PCT-094-07925-38

34 47 19.3 148 2 US-08-888-497-36

35 47 19.3 148 4 US-09-362-230-36

36 47 19.3 148 5 PCT-094-07926-36

37 47 19.3 222 1 US-08-126-593A-2

38 47 19.3 222 1 US-08-454-039A-2

39 47 19.3 349 4 US-08-462-467B-18

40 47 19.3 554 4 US-08-462-467B-22

41 47 19.3 730 1 US-08-420-235B-17

42 47 19.3 730 4 US-08-73-624-17

43 47 19.3 730 5 PCT-US95-10194-17

44 47 19.3 830 4 US-01-562-737-39

45 47 19.3 869 2 US-08-483-101-15

ALIGNMENTS

Minimum Match 0%

Maximum Match 0%

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RESULT 2
US-09-150-741-2
; Sequence 2, Application US/09150741
; Patent No. 6183996
GENERAL INFORMATION:
APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence Encoding Carbamoyl Phosphate
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/09150.741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
EARLIER APPLICATION NUMBER: AU93/00617
EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 084446, 855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 2391
TYPE: PRT
FEATURE:
ORGANISM: Artificial sequence
OTHER INFORMATION: Description of Artificial Sequence: protein
US-09-150-741-2

Query Match 24.9%; Score 60.5; DB 4; Length 2391;
Best Local Similarity 34.3%; Pred. No. 12;
Matches 12; Conservative 10; Mismatches 12; Indels 1; Gaps 1;
"Qy 2 ISHFLKMEISNFIKRAHPTYI-NIYNYCEPANPSEKN 35
Db 317 INHTTLRDKMLTSEEYLUKDHNCNFNSNSDKN 351

RESULT 3
US-09-134-001C-5086
; Sequence 5085, Application US/09134001C
; Patent No. 6580370
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134, 001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055, 779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 5086
LENGTH: 101
TYPE: PRT
ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-5086

Query Match 23.0%; Score 56; DB 4; Length 101;
Best Local Similarity 35.7%; Pred. No. 1.1;
Matches 15; Conservative 5; Mismatches 18; Indels 4; Gaps 2;
"Qy 6 LKMMSSLN---FIRATPTYI-NIYNYCEPANPSEKSPSPTOYCY 43
Db 9 LKYNBINKNOLISSEBTPELENFQDQCKINKKNNKISOSTLNCY 50

RESULT 4
US-08-445-586-7
; Sequence 7, Application US/08445586

RESULT 5
US-08-445-586-2
; Sequence 2, Application US/08445586
; Patent No. 5627050
GENERAL INFORMATION:
APPLICANT: Takeshita, Sunao
APPLICANT: Ito, Toshimi
APPLICANT: otawari-Hamamoto, Yoko
APPLICANT: Aman, Egon
TITLE OF INVENTION: Bone-Related Sulfatase-Like Protein and
TITLE OF INVENTION: Process for its Production
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADRESSEE: Pinnegan, Henderson, Farabow, Garrett & Dunner
ADRESSEE: Pinnegan, Henderson, Farabow, Garrett & Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/445, 586
APPLICATION NUMBER: US/08/445, 586
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/111, 887
FILING DATE: 26-AUG-1993
APPLICATION NUMBER: JP 230030/92
FILING DATE: 28-AUG-1992
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: JP 324034/92
FILING DATE: 03-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Forman, David S.
REGISTRATION NUMBER: 33, 694
REFERENCE/DOCKET NUMBER: 02481.1322-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 554 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: Peptide
US-08-445-586-7

Query Match 22.4%; Score 54.5; DB 1; Length 554;
Best Local Similarity 40.7%; Pred. No. 14;
Matches 11; Conservative 6; Mismatches 9; Indels 1; Gaps 1;
"Qy 3 SHFLKMEISNFIKRAHPTYI-NIYNYCEP 28
Db 55 SQVVKLUPFINMRAHGTTFLNAYTNSP 81

STREET: 1300 I Street, N.W.
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3314

CURRENT APPLICATION FORM:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION NUMBER: US/08/445,586
 FILING DATE: 28-AUG-1992

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/111,887
 FILING DATE: 26-AUG-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Forman, David S.
 REGISTRATION NUMBER: 33,694
 REFERENCE/DOCKET NUMBER: 02481.1322-00000
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-408-4000
 TELEFAX: 202-408-4400
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 556 amino acids
 TYPE: amino acid
 TOPOLGY: linear
 MOLECULE TYPE: protein

SEQUENCE DATA:
 3 SHFLKMEISLNFRRAH-IPYINYCEP 28
 55 SQVVKLKFINFMRRAHGTFLNAYTNSP 81

LT 6
 8-967-024C-25
 quence 25, Application US/08967024C
 tient No. 6133011
 ERNAL INFORMATION:
 APPLICANT: Wnenit, Stephan
 APPLICANT: . STEFFENS, Gerd Josef
 APPLICANT: JANUCHA, Elke
 APPLICANT: HEINZEL-WIELAND, Regina
 TITLE OF INVENTION: Chimeric Proteins having Fibrinolytic
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Evanson, McKeown, Edwards & Lenahan
 STREET: 1200 G Street, N.W., Suite 700
 CITY: Washington
 STATE: DC
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,493
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 991,973
 FILING DATE: 17-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DiGilio, Frank S
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 8416Z
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEFAX: 516-742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 551 amino acids
 TYPE: amino acid

APPLICATION NUMBER: P 944 42 665, 8
 FILING DATE: 30-NOV-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D.
 REGISTRATION NUMBER: 26,269
 REFERENCE/DOCKET NUMBER: 148/42444
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 628-8800
 TELEFAX: (202) 628-8844
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 393 amino acids
 TYPE: amino acid

STRANDEDNESS:
 TOPOLGY: linear
 MOLECULE TYPE: protein

US-08-967-024C-25
 RESULT 7
 Query Match 22.0%; Score 53.5; DB 4; Length 393;
 Best Local Similarity 29.4%; Pred. No. 13; Mismatches 14; Indels 15; Gaps 2
 Matches 15; Conservative 7; Mismatches 14; Indels 15; Gaps 2
 ; Sequence 15, Application US/08484493
 ; Patent No. 5728381
 ; GENERAL INFORMATION:
 ; APPLICANT: Wilson, Peter J
 ; APPLICANT: Morris, Charles P
 ; APPLICANT: Anson, Donald S
 ; APPLICANT: Occhiodoro, Teresa
 ; APPLICANT: Bleilich, Julie
 ; APPLICANT: Clements, Peter R
 ; APPLICANT: Hopwood, John J
 ; TITLE OF INVENTION: GLYCOSYLATION VARIANTS OF
 ; TITLE OF INVENTION: IDURONATE 2-SULFATASE
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Scully, Scott, Murphy & Presser
 ; STREET: 400 Garden City Plaza
 ; CITY: Garden City
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 11530
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,493
 FILING DATE: 07-JUN-1995
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 991,973
 FILING DATE: 17-DEC-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: DiGilio, Frank S
 REGISTRATION NUMBER: 31,346
 REFERENCE/DOCKET NUMBER: 8416Z
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 516-742-4343
 TELEFAX: 516-742-4366
 TELEX: 230 901 SANS UR
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 551 amino acids
 TYPE: amino acid

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/967,024C
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:

APPLICANT: Stalker, D. et al.
 TITLE OF INVENTION: Plant Cellulose Synthase and Promoter
 FILE REFERENCE: 15621/01US
 CURRENT APPLICATION NUMBER: US/08/960, 048C
 CURRENT FILING DATE: 1997-10-29
 PRIOR APPLICATION NUMBER: 60/029, 987
 NUMBER OF SEQ ID NOS: 12
 SOFTWARE: FastSEQ for Windows Version 4.0
 SBQ ID NO: 8
 LENGTH: 881
 TYPE: PRT
 ORGANISM: Oryzae sativa
 US-08-060-048-8

Query Match
 Best Local Similarity 20.5%; Score 50; DB 4; Length 881;
 Matches 11; Conservative 3; Mismatches 19; Indels 0; Gaps 0;
 QY 9 ESLNFNIRHTAYINTINCEPANPSEKNSPSTQY 41
 Db 208 ETSEFFRKWVFEVKKINPEPAPENFSKIDY 240

RESULT 13
 US-08-469-486-50
 ; Sequence 50, Application US/08469486
 ; Patent No. 5739281

GENERAL INFORMATION:
 APPLICANT: Thøgersen, Hans Christian
 APPLICANT: Holte, Thor Las
 APPLICANT: Elzeroot, Michael
 TITLE OF INVENTION: Improved method for the refolding of
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version
 SOFTWARE: #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469, 658
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIORITY INFORMATION:
 PRIORITY NUMBER: 08/192, 060
 APPLICATION NUMBER: 08/192, 060
 FILING DATE: February 4, 1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06363/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 542 5070
 TELEFAX: 617 542 8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-658-50

RESULT 14
 US-08-469-658-50
 ; Sequence 50, Application US/08469658
 ; Patent No. 5917018

GENERAL INFORMATION:
 APPLICANT: Thøgersen, Hans Christian
 APPLICANT: Holte, Thor Las
 APPLICANT: Elzeroot, Michael
 TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF
 NUMBER OF INVENTION: PROTEINS
 NUMBER OF SEQUENCES: 58
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson P.C.
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version
 SOFTWARE: #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/469, 658
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIORITY INFORMATION:
 PRIORITY NUMBER: 08/192, 060
 APPLICATION NUMBER: 08/192, 060
 FILING DATE: February 4, 1994
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Paul T. Clark
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06363/002002
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617 542 5070
 TELEFAX: 617 542 8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 50:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 119 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-469-658-50

Query Match
 Best Local Similarity 20.4%; Score 49.5; DB 2; Length 119;
 Matches 14; Conservative 6; Mismatches 16; Indels 5; Gaps 2;
 QY 5 FLKMEUNFIRA-HPPININCEPANPSEKNSPSTQY 43
 Db 9 FLVLVSLTIGIAQKQPOIQVYS--RHPPENGKPNILNY 46

RESULT 15
 US-09-360-197-10
 ; Sequence 10, Application US/09360197
 ; Patent No. 6247859

APPLICANT: Lazdunski, Michel
APPLICANT: Waldmann, Rainer
TITLE OF INVENTION: Human and Rat Families of Neuronal-Acid-Sensitive
Title of Invention: Cationic Channels, Their Cloning and Applications
FILE REFERENCE: 989 6706P
CURRENT APPLICATION NUMBER: US/09/360,197
CURRENT FILING DATE: 1997-07-23
PRIOR APPLICATION NUMBER: 09/129,758
PRIOR FILING DATE: 1998-08-05
PRIOR APPLICATION NUMBER: 60/095,408
PRIOR FILING DATE: 1998-01-05
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 10
LENGTH: 533
TYPE: PRT
ORGANISM: *rattus sp.*
US-09-360-197-10



OM protein - protein search, using sw model.

Run on: March 19, 2003, 17:30:39 ; Search time 17 Seconds
 (without alignments)
 138.373 Million cell updates/sec

Title: US-09-674-975-1

Perfect score: 243

Sequence: 1 KISHEIJKMESLNFIKRAHTPY..... NCEPANPSEKNSPSTQYCVS 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 221153 seqs, 53462247 residues

Total number of hits satisfying chosen parameters: 221153

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum Match 0%

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/1/pubpa/NS08_NEW_PUB.pep:*

2: /cgn2_6/ptodata/1/pubpa/PC1_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpa/NS06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpa/NS06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpa/NS07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpa/NS07_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpa/PC08_PUBCOMB.pep:*

8: /cgn2_6/ptodata/1/pubpa/NS08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpa/NS09_NEW_PUB.pep:*

10: /cgn2_6/ptodata/1/pubpa/NS09_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpa/NS10_NEW_PUB.pep:*

12: /cgn2_6/ptodata/1/pubpa/NS10_PUBCOMB.pep:*

13: /cgn2_6/ptodata/1/pubpa/NS60_NEW_PUB.pep:*

14: /cgn2_6/ptodata/1/pubpa/NS60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1
 US-09-674-975-1
 Sequence 928, Application US/09796692
 Publication No. US20020198362A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Maunin, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND TREATMENT OF INVENTION: HEMATOLOGICAL MALIGNANCIES
 ; FILE REFERENCE: 2077-001200
 ; CURRENT APPLICATION NUMBER: US/09796,692
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,779
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 9597
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO: 928
 LENGTH: 150
 TYPE: PRT

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	212	87.2	150	9 US-09-796-692-928
2	212	87.2	150	9 US-09-796-692-933
3	212	87.2	150	9 US-09-796-692-974
4	212	87.2	150	9 US-09-796-692-983
5	212	87.2	150	9 US-09-796-692-1314
6	212	87.2	150	9 US-09-796-692-1940
7	196	80.7	146	9 US-09-796-692-852
8	184	75.7	94	9 US-09-796-692-1260
9	144	59.3	137	9 US-09-796-692-1320
10	97	39.9	141	9 US-09-796-692-820
11	61	25.3	1013	9 US-10-028-072-38
12	61.5	25.3	1013	9 US-10-121-049-38
13	61.5	25.3	1013	9 US-10-123-904-38
14	61.5	25.3	1013	9 US-10-140-470-38
15	61.5	25.3	1013	9 US-10-175-746-38
16	61.5	25.3	1013	9 US-10-176-918-38
17	61.5	25.3	1013	9 US-10-176-921-38
18	61.5	25.3	1013	9 US-10-137-865-38
19	61.5	25.3	1013	9 US-10-140-474-38

; ORGANISM: Homo sapiens
; US-09-796-692-928

Query Match 87.2%; Score 212; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KMESLNFRATHPYINYCEPANPSEKNSPSTQCY 44
Db 1 KMESLNFRATHPYINYCEPANPSEKNSPSTQCY 38

RESULT 2

US-09-796-692-933

; Sequence 933, Application US/09796692

; Publication No. US20020198362A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER

; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

; FILE REFERENCE: 2077.001200

; CURRENT APPLICATION NUMBER: US/09/796,692

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; ORGANISM: Homo sapiens
; US-09-796-692-974

Query Match 87.2%; Score 212; DB 9; Length 150;
Best Local Similarity 100.0%; Pred. No. 2.7e-20;
Matches 38; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 KMESLNFRATHPYINYCEPANPSEKNSPSTQCY 44
Db 1 KMESLNFRATHPYINYCEPANPSEKNSPSTQCY 38

RESULT 4

US-09-796-692-983

; Sequence 983, Application US/09796692

; Publication No. US20020198362A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER

; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES

; FILE REFERENCE: 2077.001200

; CURRENT APPLICATION NUMBER: US/09/796,692

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-01

PRIOR FILING DATE: 2000-05-04
 PRIORITY APPLICATION NUMBER: 60/206,201
 PRIORITY APPLICATION NUMBER: 60/218,950
 PRIORITY FILING DATE: 2000-07-14
 PRIORITY APPLICATION NUMBER: 60/222,903
 PRIORITY FILING DATE: 2000-08-03
 PRIORITY APPLICATION NUMBER: 60/223,416
 PRIORITY FILING DATE: 2000-08-04
 PRIORITY APPLICATION NUMBER: 60/223,378
 PRIORITY FILING DATE: 2000-08-07
 NUMBER OF SEQ ID NOS: 9597
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 983
 LENGTH: 150
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: variant
 LOCATION: (1)..(150)
 OTHER INFORMATION: xaa = Any amino acid
 3-09-796-692-983
 Query Match 87.2%; Score 212; DB 9; Length 150;
 Best Local Similarity 100.0%; Pred. No. 2.7e-20;
 Matches 38; Conservative 0; Mismatches 0;
 Matches 38; Mismatches 0;
 Indels 0; Gaps 0;
 Matches 38; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 RESULT 5
 -09-796-692-1314
 Sequence 1314, Application US/09796692
 Publication No. US20020198362A1
 GENERAL INFORMATION:
 APPLICANT: Gaiger, Alexander
 APPLICANT: Algate, Paul A.
 APPLICANT: Mannion, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 FILE REFERENCE: 2007.001200
 CURRENT APPLICATION NUMBER: 05/09/796,692
 CURRENT FILING DATE: 2001-03-01
 PRIORITY APPLICATION NUMBER: 60/186,126
 PRIORITY FILING DATE: 2000-03-01
 PRIORITY APPLICATION NUMBER: 60/190,479
 PRIORITY FILING DATE: 2000-03-17
 PRIORITY APPLICATION NUMBER: 60/200,545
 PRIORITY FILING DATE: 2000-04-27
 PRIORITY APPLICATION NUMBER: 60/200,545
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/200,303
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/200,779
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/200,779
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/200,999
 PRIORITY FILING DATE: 2000-05-01
 PRIORITY APPLICATION NUMBER: 60/202,084
 PRIORITY FILING DATE: 2000-05-04
 PRIORITY APPLICATION NUMBER: 60/202,084
 PRIORITY FILING DATE: 2000-05-04
 PRIORITY APPLICATION NUMBER: 60/206,201
 PRIORITY FILING DATE: 2000-05-22
 PRIORITY APPLICATION NUMBER: 60/218,950
 PRIORITY FILING DATE: 2000-07-14
 PRIORITY APPLICATION NUMBER: 60/222,903
 PRIORITY FILING DATE: 2000-08-03
 PRIORITY APPLICATION NUMBER: 60/223,416
 PRIORITY FILING DATE: 2000-08-04
 PRIORITY APPLICATION NUMBER: 60/223,378
 PRIORITY FILING DATE: 2000-08-07
 NUMBER OF SEQ ID NOS: 9597
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1940
 LENGTH: 150
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: variant
 LOCATION: (1)..(150)
 OTHER INFORMATION: xaa = Any amino acid
 US-09-796-692-1314
 Query Match 87.2%; Score 212; DB 9; Length 150;
 Best Local Similarity 100.0%; Pred. No. 2.7e-20;
 Matches 38; Conservative 0; Mismatches 0;
 Matches 38; Mismatches 0;
 Indels 0; Gaps 0;
 Matches 38; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;
 RESULT 6
 US-09-796-692-1940
 Sequence 1940, Application US/09796692
 Publication No. US20020198362A1
 GENERAL INFORMATION:
 APPLICANT: Gaiger, Alexander
 APPLICANT: Algate, Paul A.
 APPLICANT: Mannion, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 FILE REFERENCE: 2007.001200
 CURRENT APPLICATION NUMBER: US/09/796,692
 CURRENT FILING DATE: 2001-03-01
 PRIORITY APPLICATION NUMBER: 60/186,126
 PRIORITY FILING DATE: 2000-03-01
 PRIORITY APPLICATION NUMBER: 60/190,479
 PRIORITY FILING DATE: 2000-03-17
 PRIORITY APPLICATION NUMBER: 60/200,545
 PRIORITY FILING DATE: 2000-04-27
 PRIORITY APPLICATION NUMBER: 60/200,303
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/200,779
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/200,999
 PRIORITY FILING DATE: 2000-04-28
 PRIORITY APPLICATION NUMBER: 60/206,201
 PRIORITY FILING DATE: 2000-05-22
 PRIORITY APPLICATION NUMBER: 60/218,950
 PRIORITY FILING DATE: 2000-07-14
 PRIORITY APPLICATION NUMBER: 60/222,903
 PRIORITY FILING DATE: 2000-08-03
 PRIORITY APPLICATION NUMBER: 60/223,416
 PRIORITY FILING DATE: 2000-08-04
 PRIORITY APPLICATION NUMBER: 60/223,378
 PRIORITY FILING DATE: 2000-08-07
 NUMBER OF SEQ ID NOS: 9597
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO 1940
 LENGTH: 150
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: variant
 LOCATION: (1)..(150)
 OTHER INFORMATION: xaa = Any amino acid
 US-09-796-692-1940
 Query Match 87.2%; Score 212; DB 9; Length 150;
 Best Local Similarity 100.0%; Pred. No. 2.7e-20;
 Matches 38; Conservative 0; Mismatches 0;
 Matches 38; Mismatches 0;
 Indels 0; Gaps 0;
 Matches 38; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

Sequence 852, Application US/09796692
 Publication No. US20020198362A1
 GENERAL INFORMATION:
 APPLICANT: Gaiger, Alexander
 APPLICANT: Algate, Paul A.
 APPLICANT: Mannon, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 FILE REFERENCE: 2077.001200
 CURRENT APPLICATION NUMBER: US/09/795,692
 CURRENT FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 60/186,126
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 60/190,479
 PRIOR FILING DATE: 2000-03-17
 PRIOR APPLICATION NUMBER: 60/200,545
 PRIOR FILING DATE: 2000-04-27
 PRIOR APPLICATION NUMBER: 60/200,303
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,999
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/202,084
 PRIOR FILING DATE: 2000-05-04
 PRIOR APPLICATION NUMBER: 60/206,201
 PRIOR FILING DATE: 2000-05-22
 PRIOR APPLICATION NUMBER: 60/218,950
 PRIOR FILING DATE: 2000-06-14
 PRIOR APPLICATION NUMBER: 60/200,999
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/202,084
 PRIOR FILING DATE: 2000-05-04
 PRIOR APPLICATION NUMBER: 60/205,201
 PRIOR FILING DATE: 2000-05-22
 PRIOR APPLICATION NUMBER: 60/218,950
 PRIOR FILING DATE: 2000-06-07
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 852
 LENGTH: 146
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: variant
 LOCATION: (1)..(146)
 OTHER INFORMATION: Xaa = Any amino acid
 ; US-09-796-692-852
 Query Match 80.7%; Score 196; DB 9; Length 146;
 Best Local Similarity 94.7%; Pred No. 3; Le-18; 2; Indels 0; Gaps 0;
 Matches 36; Conservative 0; Mismatches 2;
 QY 7 KMESSLNFRAHTPYINTYNEPANPSEKNSPSTQYCYS 44
 Db 1 KMESLNFRAHTPYINTYNEPANPSEKNSPSTQYCYS 38
 RESULT 8
 US-09-796-692-1260
 ; Sequence 1320, Application US/09796692
 ; Publication No. US20020198362A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannon, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 ; FILE REFERENCE: 2077.001200
 ; CURRENT APPLICATION NUMBER: US/09/795,692
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 9597
 ; SEQ ID NO: 852
 ; LENGTH: 146
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (1)..(94)
 ; OTHER INFORMATION: Xaa = Any amino acid
 ; US-09-796-692-1260
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (1)..(94)
 ; OTHER INFORMATION: Xaa = Any amino acid
 ; US-09-796-692-1260
 ; Query Match 75.7%; Score 184; DB 9; Length 94;
 Best Local Similarity 89.5%; Pred No. 6.8e-17; 4; Indels 0; Gaps 0;
 Matches 34; Conservative 0; Mismatches 4;
 QY 7 KMESSLNFRAHTPYINTYNEPANPSEKNSPSTQYCYS 44
 Db 1 KMESLNFRAHTPYINTYNEPANPSEKNSPSTQYCYS 38
 RESULT 9
 US-09-796-692-1320
 ; Sequence 1320, Application US/09796692
 ; Publication No. US20020198362A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Algate, Paul A.
 ; APPLICANT: Mannon, Jane
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 ; FILE REFERENCE: 2077.001200
 ; CURRENT APPLICATION NUMBER: US/09/795,692
 ; CURRENT FILING DATE: 2001-03-01
 ; PRIOR APPLICATION NUMBER: 60/186,126
 ; PRIOR FILING DATE: 2000-03-01
 ; PRIOR APPLICATION NUMBER: 60/190,479
 ; PRIOR FILING DATE: 2000-03-17
 ; PRIOR APPLICATION NUMBER: 60/200,545
 ; PRIOR FILING DATE: 2000-04-27
 ; PRIOR APPLICATION NUMBER: 60/200,303
 ; PRIOR FILING DATE: 2000-04-28
 ; PRIOR APPLICATION NUMBER: 60/200,999
 ; PRIOR FILING DATE: 2000-05-01
 ; PRIOR APPLICATION NUMBER: 60/206,201
 ; PRIOR FILING DATE: 2000-05-22
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-06-14
 ; PRIOR APPLICATION NUMBER: 60/202,084
 ; PRIOR FILING DATE: 2000-05-04
 ; PRIOR APPLICATION NUMBER: 60/218,950
 ; PRIOR FILING DATE: 2000-07-14
 ; PRIOR APPLICATION NUMBER: 60/222,903
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: 60/223,416
 ; PRIOR FILING DATE: 2000-08-04
 ; PRIOR APPLICATION NUMBER: 60/223,378
 ; PRIOR FILING DATE: 2000-08-07
 ; NUMBER OF SEQ ID NOS: 9597
 ; SEQ ID NO: 1260
 ; LENGTH: 94
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: variant
 ; LOCATION: (1)..(94)
 ; OTHER INFORMATION: Xaa = Any amino acid

PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: 60/223,416
 PRIOR FILING DATE: 2000-08-04
 PRIOR APPLICATION NUMBER: 60/223,378
 PRIOR FILING DATE: 2000-08-07
 NUMBER OF SEQ ID NOS: 9597
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 1320
 LENGTH: 137
 TYPE: PRT
 ORGANISM: Homo sapiens

US-09-796-692-1320

RESULT 10

Sequence 820 Application US/03796692
 Publication No. US20020198362A1
 GENERAL INFORMATION:
 APPLICANT: Gaier, Alexander
 APPLICANT: Algate, Paul A.
 APPLICANT: Mannion, Jane
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
 TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
 FILE REFERENCE: 2077_001200
 CURRENT APPLICATION NUMBER: US/09/796,692
 CURRENT FILING DATE: 2001-03-01
 PRIOR APPLICATION NUMBER: 60/186,126
 PRIOR FILING DATE: 2000-03-01
 PRIOR APPLICATION NUMBER: 60/190,479
 PRIOR FILING DATE: 2000-03-17
 PRIOR APPLICATION NUMBER: 60/200,545
 PRIOR APPLICATION NUMBER: 60/200,303
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,779
 PRIOR FILING DATE: 2000-04-28
 PRIOR APPLICATION NUMBER: 60/200,999
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 60/202,084
 PRIOR FILING DATE: 2000-05-04
 PRIOR APPLICATION NUMBER: 60/200,779
 PRIOR FILING DATE: 2000-05-22
 PRIOR APPLICATION NUMBER: 60/218,950
 PRIOR FILING DATE: 2000-07-14
 PRIOR APPLICATION NUMBER: 60/222,903
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: 60/223,416
 PRIOR FILING DATE: 2000-08-04
 PRIOR APPLICATION NUMBER: 60/223,378
 PRIOR FILING DATE: 2000-08-07
 NUMBER OF SEQ ID NOS: 9597
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 820
 LENGTH: 141
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: variant
 LOCATION: (1)..(141)
 OTHER INFORMATION: Xaa = Any amino acid

Query Match 39.9%; Score 97; DB 9; Length 141;
 Best Local Similarity 94.4%; Pred. No. 2.1e-05;
 US-09-796-692-820

RESULT 11

Sequence 38 Application US/10028072
 Publication No. US20030004311A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bersini, Maureen
 APPLICANT: DeForge, Laura
 APPLICANT: Desnoyers, Luc
 APPLICANT: Flvaroff, Ellen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Sherwood, Steven
 APPLICANT: Smith, Victoria
 APPLICANT: Tumas, Daniel
 APPLICANT: Watnabe, Colin K
 APPLICANT: Wood, William
 APPLICANT: Zhang, Victoria
 TITLE OF INVENTION:
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/028,072
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/049911
 PRIOR FILING DATE: 1997-05-18
 PRIOR APPLICATION NUMBER: 60/056974
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: 60/059113
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: 60/059115
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: 60/059117
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: 60/059122
 PRIOR FILING DATE: 1997-05-17
 PRIOR APPLICATION NUMBER: 60/059184
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059352
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059588
 PRIOR FILING DATE: 1997-09-19
 PRIOR APPLICATION NUMBER: 60/059836
 PRIOR FILING DATE: 1997-09-24
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062285
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062287
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/062814
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063127
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063327
 PRIOR FILING DATE: 1997-10-27

RESULT 12
OS 10-121-049-38
; Sequence 38, Application US/10121049
; Publication No. US20030022239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/121,049
; CURRENT FILING DATE: 2003-04-12
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 38
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 877, 882
; OTHER INFORMATION: unknown amino acid
; US-10-123-904-38
; Query Match 25 3%; Score 61.5; DB 9; Length 1013;
; Best Local Similarity 35.5%; Pred. No. 7.7; Matches 11; Conservative 5; Mismatches 14; Indels 1; Gaps 627 LKAHQPY-GVQACVPCPGPTKNNKIHSLCYN 656
; QY 14 IRAHTPYININYCNPANPSEKNSSTQCY 44
; Db 627 LKAHQPY-GVQACVPCPGPTKNNKIHSLCYN 656
; RESULT 14
; US 10-140-470-38
; Sequence 38, Application US/10140470
; Publication No. US20030022331A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Beresini, Maureen
; APPLICANT: DeForge, Laura
; APPLICANT: Desnoyers, Luc
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Sherwood, Steven
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K
; APPLICANT: Wood, William
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/140,470
; CURRENT FILING DATE: 2003-05-06
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 550
; SEQ ID NO: 38
; LENGTH: 1013
; TYPE: PRT
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 877, 882
; OTHER INFORMATION: unknown amino acid
; US-10-140-470-38
; Query Match 25 3%; Score 61.5; DB 9; Length 1013;
; Best Local Similarity 35.5%; Pred. No. 7.7; Matches 11; Conservative 5; Mismatches 14; Indels 1; Gaps 627 LKAHQPY-GVQACVPCPGPTKNNKIHSLCYN 656
; QY 14 IRAHTPYININYCNPANPSEKNSSTQCY 44
; Db 627 LKAHQPY-GVQACVPCPGPTKNNKIHSLCYN 656
; RESULT 15
; US 10-175-746-38

Sequence 38, Application US/10175746
Publication No. US20030027270A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P330R1C353
CURRENT APPLICATION NUMBER: US/10/175,746
CURRENT FILING DATE: 2002-06-19
PRIOR APPLICATION removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 550
SEQ ID NO: 3B
LENGTH: 1013

TYPE: PRT
ORGANISM: Homo Sapien
FEATURE:
NAME/KEY: unsure
LOCATION: 877, 882
OTHER INFORMATION: unknown amino acid

US-10-175-746-38

Query Match 25.3%; Score 61.5; DB 9; Length 1013;
Best Local Similarity 35.5%; Pred. No. 7.7;
Matches 11; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
QY 14 I R A H T P Y I N Y I N C E A N P S E K N S P S T Q Y C Y S 44
Db 627 L K A H Q P Y - G V Q A C V P C G P G T K N N K I H S L C Y N 656

Search completed: March 19, 2003, 17:57:29
Job time : 27.5 secs

GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model.

Run on:

March 19, 2003, 17:22:00 ; Search time 13.5 Seconds
(without alignments) 313.327 Million cell updates/sec

Title: US-09-674-975-1

Sequence: 1 KISHFLKMESELNFIRAHPTV..... NCEPANPSEKNSPSTQCY'S 44

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched:

283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73;*
1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being shown and is derived by analysis of the total score distribution.

ALIGNMENTS

RESULT	1
A30586	N; Alternate names: B-lymphocyte antigen CD20 - human
	B-cell surface antigen CD20 - human
	C; Species: Homo sapiens (man)
	C; Date: 08-Jun-1989 #sequence_revision 02-Aug-1996 #text_change 22-Jun-1999
	C; Accession: A30586; JID042; A27400; S0387
	R; Tedder, T.F.; Kleijman, G.; Schlossman, S.F.; Saito, H.
	J. Immunol. 142, 2560-2568, 1990
	A; Title: Structure of the gene encoding the human B lymphocyte differentiation antigen
	A; Reference number: A30586; MUID:89176281; PMID:2466899
	A; Accession: A30586
	A; Molecule type: DNA
	A; Residues: 1-297 <TIED>
	A; Note: the authors translated the codon ATG for residue 148 as His, TCA for residue
	R; Stamenkovic, I.; Seed, B.
	J. Exp. Med. 167, 1971-1980, 1988
	A; Title: Analysis of two cDNA clones encoding the B lymphocyte antigen CD20 (B1-Bp35)
	A; Reference number: JI0042; MUID:88258386; PMID:3260267
	A; Accession: JI0042
	A; Molecule type: mRNA
	A; Residues: 1-297 <STA>
	A; Cross-references: GB:X12530; NID:929773; PIDN:CAA31046.1; PID:929774
	R; Tedder, T.F.; Streuli, M.; Schlossman, S.F.; Saito, H.
	Proc. Natl. Acad. Sci. U.S.A. 85, 208-212, 1988
	A; Title: Isolation and structure of a cDNA encoding the B1 (CD20) cell-surface antigen
	A; Reference number: A27400; MUID:88124792; PMID:2448768
	A; Accession: A27400
	A; Molecule type: mRNA
	A; Residues: 1-297 <TE2>
	A; Cross-references: GB:M27394; GB:J03574; NID:9179307; PIDN:AAA35581.1; PID:9179308
	R; Einfeld, D.A.; Brown, J.P.; Valentine, M.A.; Clark, E.A.; Ledbetter, J.A.
	EMBO J. 7, 711-717, 1988
	A; Title: Molecular cloning of the human B cell CD20 receptor predicts a hydrophobic p
	A; Reference number: S00387; MUID:88283639; PMID:2456210
	A; Accession: S00387
	A; Molecule type: mRNA
	A; Residues: 1-12, L, 14-297 <EIN>
	A; Cross-references: EMBL:X07203; NID:929775; PIDN:CAA30179.1; PID:929776
	A; Experimental source: Daudi cells
	C; Comment: This protein appears not to be glycosylated. Isoforms of varying molecular
	C; Genetics: This protein plays an important role in B cell activation.
	A; Gene: GDB:CD20
	A; Cross-references: GB:119761; OMIM:112210
	A; Map position: 11q12-11q13.1
	C; Superfamily: B-cell surface antigen CD20
	C; Keywords: B-cell; phosphoprotein; transmembrane protein
	F; 1-51/Domain: intracellular #status predicted <Cyt>
	F; 52-103/Domain: transmembrane #status predicted <Cyt2>
	F; 104-116/Domain: intracellular #status predicted <Cyt2>

Result	No.	Score	Query	Match Length	DB	ID	Descriptor
1	243	100.0	297	1	A30586		B-Cell surface antigen CD20 - human
2	160	65.8	291	2	A30586		B-cell surface antigen CD20; B1
3	61	70.2	292	2	D69426		antibody
4	60.5	24.9	2391	2	T18410		PIR
5	57.5	23.7	443	2	RRCGNV		PIR
6	56.5	23.3	1643	1	D69426		PIR
7	56	23.0	2425	2	E88098		PIR
8	56	23	711	2	E88098		PIR
9	55	22.8	112	2	S35880		PIR
10	55.5	22.8	2150	2	T32497		PIR
11	54.5	22.4	547	2	T0077		PIR
12	54	22.2	253	2	F69134		PIR
13	54	22.2	329	2	H71192		PIR
14	54	22.2	337	2	T28992		PIR
15	54	22.2	437	2	B81519		PIR
16	54	22.2	447	2	F72021		PIR
17	54	22.2	447	2	A8603		PIR
18	53	21.8	2091	2	A97077		PIR
19	53	21.8	332	2	C95150		PIR
20	53	21.8	4981	2	T18410		PIR
21	52.5	21.6	117	2	S67095		PIR
22	52.5	21.6	331	2	T2873		PIR
23	52.5	21.6	604	2	S39885		PIR
24	52	21.4	411	2	S58105		PIR
25	52	21.4	532	2	JC6170		PIR
26	52	21.4	650	2	T46660		PIR
27	52	21.4	1776	2	T21172		PIR
28	51.5	21.2	438	2	G95578		PIR
29	51.5	21.2	551	2	S01793		PIR

F:117-141/Domain: transmembrane #status predicted <TM3>
 F:142-185/Domain: extracellular #status predicted <EXT>
 F:186-212/Domain: transmembrane #status predicted <TM4>
 F:213-297/Domain: intracellular #status predicted <CYT3>
 F:167-183/disulfide bonds: #status predicted

RESULT 2
A30558
B-cell surface antigen CD20 homolog - mouse
N1Alternate names: B-cell differentiation antigen Ly-44
C1Species: Mus musculus (house mouse)
C1Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 07-Feb-1997
C1Accession: A30558
R: Tedder, T.F.; Kleijman, G.; Disteche, C.M.; Adler, D.A.; Schlossman, S.F.; Saito, H.
J: Immunol. 141, 4388-394, 1988

A; Reference number: A30558; NUID:89067519; PMID:24611992
A; Accession: A30558
A; Status: not compared with conceptual translation
A; Molecule type: mRNA
A; Residues: 1-291 <TED>
; Genetics:
A; Map position: 19
C; Superfamily: B-cell surface antigen CD20

Query Match 65.8%; Score 160; DB 2; Length 291;
 Best Local Similarity 65.1%; Pred. NO. 7, 2e-13;
 Matches 28; Conservative 6; Mismatches 9; Indels 0; Gaps. 0
 QY 2 ISHLKLMESSLNFRAINTYIINYCEPANSEKNSPSTOCYS 44
 :|||||| | : |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 137 LSHFLKMRRELQIQTSKVYDIDCEPNSSEKNSPSTOCNS 179

RESULT 3
D86469
protein PI2K21.12 [Imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: D86469
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; Whitehead, C.; O'Farrell, P.H.

Query Match 25.1%; Score 61; DB 2; Length 702;
 Best Local Similarity 35.5%; Pred. No. 8 2;
 Matches 11; Conservative 8; Mismatches 12; Indels 0; Gaps

QY 14 TRAHTPYINTYNECEPANPSEKNSPSTOYCYS 4.
Db 624 VRAHTPNNSNLFSCLWNEVERFTPDRDLSFA 6

RESULT 4
T18410 carbamoyl-phosphate synthase (glutamine-hydrolyzing) (EC 6.3.5.5) II - malaria parasi
C.Species: *Plasmodium falciparum*
C.Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jun-2000

Al: Molecule type: DNA
 A1: Residues: 1-2391 <P10>
 A1: Cross-references: EMBL:132150; NID:9476023; PID:9476024; PIDN:AAA29522; 1
 C: Superfamily: rudimentary enzyme; aspartate/ornithine carbamoyltransferase homology; carbamoyl-phosphoribosyl transferase (glutamine hydrolyzing) large chain homology; carbamoyl-p
 C: Keywords: ligase

RESULT 5
S44786 D2007.5 protein - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 28-Sep-1994 #sequence_revision 12-May-1995 #text_change 23-Mar-2001
C;Accession: S44786
R;Favell, A.D. 1995

A: Description: Sequence of the *C. elegans* cosmid D2007.
A: Reference number: S44619
A: Accession: S44619
A: Status: Preliminary
A: Molecule type: DNA
A: Residues: 1-443 <FAV>
A: Cross-references: EMBL:LI16560; NID:9289666; PDB:9289666
C: GenBank ID: M32143
C: GenBank Version: 1
C: GenBank Date: 1993-07-20
C: GenBank Title: C. elegans cosmid D2007
C: GenBank Author: *WormBase*
C: GenBank URL: <http://www.wormbase.org>

Query Match 23.7%; Score 57.5; DB 2; Length 443;
 Best Local Similarity 45.7%; Pred. No. 14;
 Matches 16; Conservative 7; Mismatches 5; Indels 7; Gaps 3;
 Qy 10 S|N|F|R|A|T|T|P|Y|I|N|T|---Y|N|C|E|P|A|N|P|S|E|N|K|P|S|T| 39
 Dr 106 S|G|A|N|P|E|N|P|S|E|N|K|P|S|T|---Y|N|C|E|P|A|N|P|S|E|N|K|P|S|T| 219
 A; Intron; 25/3; 19/2; 250/3; 321/1; 335/3; 419/3
 C; Superfamily: Caenorhabditis elegans D2007.5 protein

genomic polyprotein - narcissus mosaic virus
N:Alternate names: RNA nucleotidyltransferase (RNA-directed); RNA replicase
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: narcissus mosaic virus

C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 19-Jan-2001
C;Accession: JN0470
R;Zuidema, D.; Lintorst, H.J.M.; Huisman, M.J.; Asjes, C.J.; Bol, J.F.
J. Gen. Virol. 70, 267-276, 1989

A;Title: Nucleotide sequence of narcissus mosaic virus RNA.
 A;Reference number: JT0470; MUID:89279206; PMID:2732689
 A;Molecule type: genomic RNA
 A;Residues: 1-1643 <ZUI>
 C;Superfamily: eggplant mosaic virus RNA-directed RNA polymerase
 C;Keywords: ATP; nucleotide binding; nucleotidyltransferase; P-loop; RNA biosynthesis; RNA; 875; Region: nucleotide binding motif A (P-loop)
 F;931-935;Region: nucleotide binding motif B
 F;874/Binding site: ATP (Lys) #status predicted

Query Match 23.3%; Score 56.5; DB 1; Length 1643;
 Best Local Similarity 26.9%; Pred. No. 75;
 Matches 14; Conservative 11; Mismatches 6; Indels 21; Gaps 3;

Qy 4 HFLKMESLNFIRAHPTYI-----NIVNCEPAN-PEBKNSPSTQY 41
 Db 1107 YWAKLES-----TPYLKAFIDTYRDERKETEVINSQNSOPASAEPEAPATHF 1151

RESULT 7

D69426 surface layer protein B (sl9B-2) homolog - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Accession: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
 C;Date: 05-Dec-1997
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, J.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirnness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.; Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.; Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon A;Accession: D69426
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-2425 <KLE>
 A;Cross-references: GB:AE001006; GB:AE000782; NID:92689329; PIDN:AA89834.1; PID:9264915

Query Match 23.3%; Score 56.5; DB 2; Length 2425;
 Best Local Similarity 30.0%; Pred. No. 1.1e+02;
 Matches 15; Conservative 9; Mismatches 19; Indels 7; Gaps 2;

Qy 1 KISIPLKMESLNFIRAHPTYIINYI---CEPANPSE---KNPSSTQCY 43
 Db 1764 KISSFLAARATEEVRTSPEVEVYISVNLIEVNAEFLALRNQMPDFY 1813

RESULT 8

E85998 hypothetical protein At4g09630 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: E85998
 C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-777, 1999
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
 A;Reference number: A85001; MUID:20033488; PMID:10617198
 A;Accession: E85998
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-711 <STO>
 A;Cross-references: GB:NC_001268; NID:97267658; PIDN:CA878086.1; GSPDB:GN00140
 C;Genetics: A;Gene: At4g09630
 A;Map position: 4

Query Match 23.0%; Score 56; DB 2; Length 711;
 Best Local Similarity 32.3%; Pred. No. 36;
 Matches 10; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

Qy 14 IAHPTPYINYNCEPANPSEKNSSTQYYS 44
 Db 632 VREHTPMNSLNFSCLMFNEVERFTPRDQLSFA 662

RESULT 9

S35880 submitted to the EMBL Data Library, July 1993
 A;Reference number: S35878
 A;Accession: S35880
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-112 <HON>
 A;Cross-references: EMBL:Z24758; NID:9395351; PIDN:CA80884.1; PID:9395352

Query Match 22.8%; Score 55.5; DB 2; Length 112;
 Best Local Similarity 33.3%; Pred. No. 6;
 Matches 13; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

Qy 5 FLKMESLNFIRAHPTYIINYI---CEPANPSEKNSSTQY 42
 Db 46 FSVIRAKNVEATSRYHNFSRLEGSSPSELROPIQPC 84

RESULT 10

T32497 hypothetical protein C08G9.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
 C;Accession: T32497
 R;Geisel, C.; Stellwies, L.
 A;Description: The sequence of C. elegans cosmid C08G9.
 A;Reference number: Z21179
 A;Accession: T32497
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: DNA
 A;Residues: 1-2150 <GEI>
 A;Cross-references: EMBL:AF036687; PIDN:AA88311.1; GSPDB:GN00022; CESP:C08G9.2
 A;Experimental source: strain Bristol N2; clone C08G9
 C;Genetics:
 A;Gene: CESP:C08G9.2
 A;Map position: 4
 A;Introns: 242/1; 306/1; 340/3; 485/1; 545/1; 736/2; 791/1; 829/1; 886/3; 942/1; 1079
 T00977

Query Match 22.8%; Score 55.5; DB 2; Length 2150;
 Best Local Similarity 41.2%; Pred. No. 1.3e+02;
 Matches 14; Conservative 4; Mismatches 15; Indels 1; Gaps 1;

Qy 11 LNFRIRAHPTYI-NIVNCEPANPSEKNSSTQYCY 43
 Db 610 LNFRCPAGEPYISSNAGAESTKDEECPTSTHWCH 643

RESULT 11

probable Pectinesterase At2926440 [imported] - Arabidopsis thaliana
 C;Species: Arabidopsis thaliana (mouse-ear cress)
 C;Accession: T00977; E84660
 R;Rounseley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K;Rounseley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K;Submitted to the EMBL Data Library, April 1998
 A;Description: Arabidopsis thaliana chromosome II BAC T90J22 genomic sequence.
 A;Reference number: Z14161
 A;Accession: T00977
 A;Status: translated from GB/EMBL/DBJ

Qy	3 SHFLKMEISLNFRTRAHTP-YINTYNECPANPSERK-----NSPSTQCY 43
Db	209 SYIQLKSQKLQLPKDSDYYDLRSCSTT--AKFSFSFNPLADFCY 253

Search completed: March 19, 2003, 17:22:42
Job time : 17.5 secs

Job time : 17.5 secs



GenCore version 5.1.4_P5_4578
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OM protein - protein search, using sw model.

Run on: March 19, 2003, 17:21:01 ; Search time 7.5 Seconds

(without alignments)
243.328 Million cell updates/sec

Title: US-09-674-975-1

Perfect score: 243

Sequence: 1 KISHFLKMESELNFIRAHPTV..... NCEPANPSEKNSPSTQYCVS 44

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq. length: 0
Maximum DB seq. length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Swissprot; 40; *

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match Length	DB ID	Description
1	243	100.0	297	1 CD20_HUMAN	P11836 homo sapien
2	160	65.8	291	1 CD20_MOUSE	P19437 mus musculus
3	57.5	23.7	443	1 YLM5_CAEEL	P44379 caenorhabditis elegans
4	56.5	23.3	1643	1 RRP0_NMV	P15095 narcissus macrophyllus
5	55.5	22.8	112	1 YARO_ICMV	Q08593 Indian cassia
6	52.5	21.6	584	1 SYD_BUCA	P01432 buchnera apicalis
7	52	21.4	411	1 CUF1_SCHPO	Q09728 schizosaccharomyces pombe
8	52	21.4	532	1 SREP_PENCH	P02259 penicillium
9	52	21.4	650	1 SC02_NEUDER	Q01277 neurospora crassa
10	51.5	21.1	119	1 B2MG_PITR	Q077531 pithecia irrorata
11	51.5	21.2	119	1 B2MG_SATIR	Q077534 satyrus atlanticus
12	51.5	21.2	416	1 NAP5_HUMAN	Q14513 homo sapien
13	51.5	21.0	551	1 ARS_HEPU	P14000 hemicentrotus pulcherrimus
14	51	21.0	426	1 VGF_BPG4	P02642 bacteriophaga
15	51	21.0	462	1 K6PF_METUA	Q28999 methanococcus
16	51	21.0	2109	1 PGCL_CHICK	P07899 gallus gallus
17	50.5	20.8	119	1 B2MG_ALOSE	Q077523 alouatta senilis
18	50.5	20.8	119	1 B2MG_CALEM	Q077521 callithrix jacchus
19	50.5	20.8	119	1 B2MG_CEBPV	Q077535 cebula pygmaea
20	50.5	20.8	288	1 CH1P_BETV0	P02820 beta vulgaris
21	50.5	20.8	453	1 DNAA_STAAM	P49994 staphylococcus
22	50.5	20.8	1587	1 TOP2_PENCH	Q28989 penicillium
23	50	20.6	119	1 B2MG_ATPEA	Q077536 atelopus panamensis
24	50	20.6	119	1 B2MG_CACHE	Q077533 cacaoyer
25	50	20.6	119	1 B2MG_CALHO	Q077529 callicebus
26	50	20.6	119	1 B2MG_CALMA	Q077522 callithrix
27	50	20.6	119	1 B2MG_CALPN	Q077528 callicebus
28	50	20.6	119	1 B2MG_CALPO	Q077526 callicebus
29	50	20.6	119	1 B2MG_LAGIA	Q077530 callicebus
30	50	20.6	119	1 B2MG_LAGIA	Q077525 lagothrix lagotricha
31	50	20.6	119	1 B2MG_LIEOCH	Q077519 leontopithecus
32	50	20.6	272	1 TRA2_DROIT	Q02008 drosophila
33					P08767 bacteriophaga

ALIGNMENTS

RESULT 1	ID	CD20_HUMAN	STANDARD;	PRT;	297 AA.
	CD20_HUMAN	P11836; P08984; Q13963;			
	AC	01-Nov-1988 (Rel. 09, Created)			
	DT	01-OCT-1989 (Rel. 12, Last sequence update)			
	DT	15-JUN-2002 (Rel. 41, Last annotation update)			
	DE	B-1-lymphocyte antigen CD20 (B-lymphocyte surface antigen B1) (Leu-15) (Bp35).			
	DE	(Bp35).			
	GN	MS411 OR CD20.			
	OS	Homo sapiens (Human).			
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.			
	OC	OX			
	OX	NCBI_TaxID=9606;			
	RN	[1] J. Exp. Med. 167:1975-1980(1988).			
	RP	[2] R.			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE:88124792; PubMed=2448768;			
	RA	Teodor T.F., Strelutti M., Schlossman S.F., Saito H.			
	RT	"Isolation and structure of a cDNA encoding the B1 (CD20) cell-surface antigen of human B lymphocytes."			
	RT	antigen of human B lymphocytes."			
	RT	Proc. Natl. Acad. Sci. U.S.A. 85:208-212(1988).			
	RL	[3]			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE:8917281; PubMed=2466899;			
	RA	Teodor T.F., Klejman G., Schlossman S.F., Saito H.			
	RT	"Structure of the gene encoding the human B lymphocyte differentiation antigen CD20 (B1)."			
	RT	J. Immunol. 142:2560-2568(1989).			
	RL	[4]			
	RP	SEQUENCE FROM N.A.			
	RX	MEDLINE:88283639; PubMed=2456210;			
	RA	Field D.A., Brown J.P., Valentine M.A., Clark E.A., Ledbetter J.A.;			
	RT	"Molecular cloning of the human B cell CD20 receptor predicts a hydrophobic protein with multiple transmembrane domains."			
	RT	EMBO J. 7:711-717(1988).			
	RL	[5]			
	RP	SEQUENCE FROM N.A.			
	RC	STRUCTURE-LYMPH.			
	RC	Straubberg R.;			
	RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.			
	CC	-I- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE REGULATION OF B-CELL ACTIVATION AND PROLIFERATION.			
	CC	-I- SUBCELLULAR LOCATION: Integral membrane protein.			
	CC	-I- PHOSPHORYLATED. MIGHT BE FUNCTIONALLY REGULATED BY PROTEIN KINASE(S).			
	CC	-I- SIMILARITY: BELONGS TO THE MS4A FAMILY.			
	CC	-I- DATABASE: NAME=NOTECD; GUIDE=CD20; ENTRY=WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROTC/CD20.HTML".			

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CC EMBL; X112530; CAA31046.1; --

DR EMBL; M27394; AAA335581.1; --

DR EMBL; M27595; ; NOT_ANNOTATED_CDS.

DR EMBL; L23419; AAA88911.1; --

EMBL; L23415; AAA88911.1; JOINED.

DR EMBL; L23416; AAA88911.1; JOINED.

DR EMBL; L23417; AAA88911.1; JOINED.

DR EMBL; X07203; CAA30179.1; --

DR EMBL; X07204; CAA30180.1; --

DR EMBL; BC002807; AAH02807.1; --

DR PIR; A27400; A27400.

DR PIR; JL0042; JL0042.

DR PIR; A30586; A30586.

DR PIR; S00387; S00387.

DR Gene; HGNC; 7315; MSA1.

DR MIM; 112210; .

KW B-cell; Transmembrane; Phosphorylation; Cytoplasmic (potential).

FT DOMAIN 1 63 POTENTIAL.

FT TRANSEM 64 84 POTENTIAL.

FT TRANSEM 85 105 POTENTIAL.

FT TRANSEM 121 141 POTENTIAL.

FT TRANSEM 189 209 POTENTIAL.

FT DOMAIN 210 297 CYTOPLASMIC (potential).

FT DISULFID 81 167 PROBABLE.

FT DISULFID 167 183 PROBABLE.

FT DISULFID 111 220 PROBABLE.

FT CONFLICT 13 13 P -> L (IN REF. 4).

FT CONFLICT 71 71 M -> T (IN REF. 3).

SQ SEQUENCE 297 AA; 33077 MW; AC5420F88626BD1 CRC64;

Query Match 100%; Score 243; DB 1; Length 297; Best Local Similarity 100%; Pred. No. 9.5e-25; Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KISHLKMESELNFRAHTPYNIYNEPANSEKNSPSTQCY 44

Db 142 KISHLKMESELNFRAHTPYNIYNEPANSEKNSPSTQCY 185

RESULT 2

CD20_MOUSE

ID CD20_MOUSE STANDARD; PRT; 291 AA.

AC P19437; .

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE B-cell surface protein CD20 homolog (B-cell differentiation antigen LY-44).

DE MS4A1 OR CD20 OR LY-44 OR MS442.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.

NCBI_TAXID=10090; [1]

RP SEQUENCE FROM N.A. MEDLINE=88067519; PubMed=2461992; Tedder T.F., Klejman G., Distefano C.M., Adler D.A., Schlossman S.F., Saito H.; "Cloning of a complementary DNA encoding a new mouse B lymphocyte differentiation antigen, homologous to the human B1 (CD20) antigen, and localization of the gene to chromosome 19."; J. Immunol. 141:4388-4394(1988). [2]

RP SEQUENCE FROM N.A. STRAIN=C57BL/6U; TISSUE=Thymus;

CC EMBL; KUEHL P., LEWIS S., MATSUO Y., NIKKIDO I., PESOLE G., QUACKENBUSH J., SCHIRML L.M., STAUBLI F., SUZUKI R., TONITA M., WAGNER L., WASHIO T., SAKAI K., OKIDO T., FURUO M., AONO H., BALDARELLI R., BARSH G., BLAKE J., BOFFELLI D., BOJUNGA N., CARNICCI P., DE BONALDO M.F., BROWNSTEIN M.J., BULT C., FLETCHER C., FUJINCI M., GARIBOLDI M., GUSTINICH S., HILL D., HOFMANN M., KANIYA M., LEE N.H., LYONS P., MARCIONI L., MASHIMA J., MAZZARELLI J., MOMBARTS P., NORDONI P., RING B., RINOWALD M., RODRIGUEZ L., SAKAMOTO N., SASAKI H., SATO K., SCHOENBACH C., SEYA T., SHIBATA Y., STORCH K.-F., SUZAKI H., TOYO-OKA K., WANG K.-H., WEITZ C., WHITAKER C., WILMING L., WYNSHAW-BORIS A., YOSHIDA K., HASEGAWA Y., KAWAJI H., KOHTUKI S., RAHAYASHI Y.; "Functional annotation of a full-length mouse cDNA collection.", NATURE 409:685-690(2001).

CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE REGULATION OF B-CELL ACTIVATION AND PROLIFERATION.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.

CC -1- PIM: PHOSPHORYLATED BY THE MSA1 FAMILY.

CC -1- SIMILARITY: BELONGS TO THE MSA1 FAMILY.

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CC EMBL; M62541; AAA37394.1; --

DR EMBL; AK017903; BAB30996.1; --

DR PIR; A30586; A30586.

DR MGD; MGI:88321; MSA2.

KW B-cell; Transmembrane; Phosphorylation; Cytoplasmic (potential).

FT DOMAIN 1 44 POTENTIAL.

FT TRANSEM 45 65 POTENTIAL.

FT TRANSEM 69 89 POTENTIAL.

FT TRANSEM 112 132 POTENTIAL.

FT TRANSEM 183 203 POTENTIAL.

FT DOMAIN 204 291 CYTOPLASMIC (potential).

SQ SEQUENCE 291 AA; 31958 MW; DF478EC02C5C16FC CRC64;

Query Match 65.8%; Score 160; DB 1; Length 291; Best Local Similarity 65.1%; Pred. No. 7.9e-14; Matches 28; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Oy 2 ISHLKMESELNFRAHTPYNIYNEPANSEKNSPSTQCY 44

Db 137 LSHFLKMRRELQISKPVWIDCEPSNSSEKNSPSTQCY 179

RESULT 3

YLM5_CAEEL

ID YLM5_CAEEL STANDARD; PRT; 443 AA.

AC P34379; .

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical protein D2007.5 in chromosome III.

GN D2007.5.

OS Caenorhabditis elegans.

OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderrinae; Caenorhabditis.

NCBI_TAXID=6239; [1]

RP SEQUENCE FROM N.A. STRAIN=BRISTOL N2;

RC

OS *Buchnera aphidicola* (subsp. *Schizaphis graminum*)
 OC Bacteria; Proteobacteria; gamma subdivision; *Buchnera*.
 OX NCBI_TAXID=98794;
 RN [1]
 RP SQUENCE FROM N.A.
 RA Thao M.L., Baumann P.:
 RT "Nucleotide sequence of a DNA fragment from *Buchnera aphidicola* (Aphid endosymbiont) containing the genes *aspS-txb-sers-serC-aroA-ipsA-hmd-tpla*;"
 RT Curr. Microbiol. 35:68-69(1997).
 CC -I CATALYTIC ACTIVITY: ATP + L-aspartate + tRNA(Asp) = AMP +
 CC diphosphate + L-aspartyl-tRNA(Asp).
 CC -I SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -I SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
 CC -I SIMILARITY: BELONGS TO CLASS II AMINOCYL-TRNA SYNTHETASE FAMILY.
 CC
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 CC
 CC
 EMBL; L43549; AR05432.1; -.
 DR EMBL; P21889; IFR0.
 DR InterPro; IPR002106; AATRNA_ligaseI.
 DR InterPro; IPR004524; ASPS_bact.
 DR InterPro; IPR004115; GAD_dom.
 DR InterPro; IPR004364; tRNA-synt_2.
 DR InterPro; IPR003312; tRNA-synt_LasP.
 DR InterPro; IPR004365; tRNA_antI.
 DR Pfam; PF00152; tRNA-synt_2; 2.
 DR Pfam; PF01336; tRNA_antI; 1.
 DR Prints; PRO1042; TRNA-SYNTTHASP.
 DR TIGR00459; ASPS_bact; 1.
 DR PROSITE; PS50862; AA_ Ligase_II; 1.
 KW Aminocycl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
 FT DOMAIN 79 84
 FT POL ASN;
 SQ SEQUENCE 584 AA; 67824 MW; F318DPA154780E7 CRC64;
 Query Match 21.6%; Score 52.5; DB 1; Length 584;
 Best Local Similarity 34.0%; Pred. No. 25; Mismatches 16; Indels 7; Gaps 3;
 Matches 16; Conservative 8; MisMatches 16; Indels 7; Gaps 3;
 OY 1 KISHIFLU--MESLNFRAHTPYVINYCEPAN--PSEKNSPSTQY 41
 Db 141 KITHURIFMENKFNFIDIEPFLTKSTPEGARDILVLPs-RNIPGNFY 186
 RESULT 7
 CUFFL_SCHPO
 ID CUFFL_SCHPO STANDARD; PRT; 411 AA.
 AC 009720;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Metal-binding regulatory protein cuffl.
 DE CUFFL OR SPAC31A2.11C.
 OS Schizosaccharomyces pombe (Fission yeast),
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomyces;
 OX NCBI_TAXID=4896;
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=FY254;
 RX MEDLINE=20062836; PubMed=1053913;
 RA Labbe S., Pena M.M.O., Fernandes A.R., Thiele D.J.;
 RT "A copper-sensing transcription factor regulates iron uptake genes in
 Schizosaccharomyces pombe";
 RL J. Biol. Chem. 274:36252-36260(1999).
 RESULT 8
 SREP_PENCH
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgourou S., Peat N., Hayles J., Baker S., Basman D., Bowman S.,
 RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
 RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J.S., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odeil C.,
 RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Robish S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robish J., Warren T., Whitehead S.,
 RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Fritzze C., Holzer E., Moestl D., Hilbert H.,
 RA Zymark K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Caudie S.J., Dreano S., Goux S., Hilaire V., Mottier S.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
 RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.,
 RT "The genome sequence of Schizosaccharomyces pombe.",
 RL Nature 415:871-880(2002).
 CC -I FUNCTION: COPPER-SENSING TRANSCRIPTION FACTOR THAT REGULATES IRON UPTAKE GENES.
 CC -I SUBCELLULAR LOCATION: Nuclear (Potential).
 CC -I SIMILARITY: CONTAINS 1 COPPER-FIST DNA-BINDING DOMAIN.
 CC
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 CC
 CC
 DR EMBL; AF175404; AAD51063.1; -.
 DR EMBL; AJ243832; CAB2304.1; -.
 DR EMBL; Z50113; CAA90469.1; -.
 DR InterPro; IPR010103; Copper-fist.
 DR Pfam; PF00649; COPPER-FIST; 1.
 DR Prints; PRO0617; COPPERFIST.
 DR PRODOM; PDO09050; COPPERFIST.
 DR SMART; SM04112; Cu_FIST; 1.
 DR PROSTRE; PS01119; Cu_FIST; 1.
 DR PROSTRE; PS50073; COPPER_FIST; 1.
 DR PROSTRE; PS50073; COPPER_FIST; 2; 1.
 KW TRANSCRIPTION _REGULATION; DNA_BINDING; Copper; Nuclear protein.
 FT DNA_BIND 1 40 COPPER-FIST.
 FT METAL 11 11 ZINC (BY SIMILARITY).
 FT METAL 14 14 ZINC (BY SIMILARITY).
 FT METAL 23 23 ZINC (BY SIMILARITY).
 FT METAL 25 25 ZINC (BY SIMILARITY).
 SQ SEQUENCE 411 AA; 45472 MW; DB10887/B65D5699 CRC64;
 Query Match 21.4%; Score 52; DB 1; Length 411;
 Best Local Similarity 35.7%; Pred. No. 19; Mismatches 15; Conservative 2; MisMatches 2; Indels 0; Gaps 0;
 Matches 15; Conservative 2; MisMatches 2; Indels 0; Gaps 0;
 OY 3 SHFLKNEFLNIFRAHTPYVINYCEPAN--PSEKNSPSTQYCS 44
 Db 167 SQFLPIEKLSNVAYPPNNVNLKSPYQQPTNFPPEIQLNYS 208
 RESULT 8
 SREP_PENCH

DT 15-JUL-1998 (Rel. 36, last annotation update)
 DE Arylsulfatase precursor (EC 3.1.6.1) (Aryl-sulfate sulphohydroxylase)
 DE (ARS)
 OS Hemicentrotus pulcherrimus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Ectotherozoa; Echinozoa;
 OC Echinoidea; Bivalvia; Echinoidea; Strongylocentrotidae;
 OC Hemicentrotus.
 OX NCBI_TaxID=650;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Pluteus;
 RX MEDLINE=8903699; PubMed=3181160;
 RA Sasaki H., Yamada K., Akasaka H., Suzuki K., Saito A., Saito M.,
 RA Shimada H.;
 RT "cDNA cloning, nucleotide sequence and expression of the gene for
 arylsulfatase in the sea urchin (Hemicentrotus pulcherrimus)
 embryo.";
 RL Eur. J. Biochem. 177:9-13(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90093130; PubMed=2558936;
 RA Yamada K., Akasaka K., Shimada H.;
 RT "Structure of sea urchin arylsulfatase gene.";
 RL Eur. J. Biochem. 186:405-410(1989).
 CC --!- FUNCTION: MAY BE A STRUCTURAL COMPONENT OF THE EXTRACELLULAR
 MATRICES INVOLVED IN CELL MOVEMENT DURING MORPHOGENESIS.
 CC --!- CATALYTIC ACTIVITY: A phenol sulfate + H(2)O = a phenol + sulfate.
 CC --!- SUBCELLULAR LOCATION: IN BOTH THE CYTOPLASM AND THE EXTRACELLULAR
 MATRICES.
 CC --!- SIMILARITY: BELONGS TO THE SULFATASE FAMILY.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X17015; CAA4881.1; --.
 DR PIR; S01793; S01793.
 DR PIR; S07089; S07089.
 DR HSSP; P15289; IAUK.
 DR InterPro; IPR000917; Sulfatase.
 DR Pfam; PF00884; Sulfatase; I.
 DR PROSITE; PS00523; SULFATASE_1; 1.
 DR PROSITE; PS00149; SULFATASE_2; 1.
 KW Hydrolase; Signal; Glycoprotein; Extracellular matrix.
 FT SIGNAL 1 20 ARYL-SULFATASE.
 FT CHAIN 21 551 - BLOCKED.
 FT MOD_RES 21 21 100 100 2-AMINO-3-OXOPROPIONIC ACID (BY
 FT ACT_SITE 158 158 2-SIMILARITY).
 FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 296 296 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 551 AA: 60952 MN: 54C1AAC14D6710C9 CRC64;
 Query Match 21.2%; Score 51.5; DB 1; Length 551;
 Best Local Similarity 24.4%; Pred. No. 32; Mismatches 20; Indels 1; Gaps 1;
 Matches 10; Conservative 10; PRT; 426 AA.
 QY 3 SHFLKMESLNFTIHAHTPYNTYCEPANPSEKPSKPTOYC 43
 DB 170 AHPFNGHDFVQHNLPPFTNSWCGDDTG-LHKQDPDSRCY 209
 RESULT 15
 KGP-META ID KGP-METJA STANDARD: PRT; 462 AA.
 ID Q58999; DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE ADP-specific phosphofructokinase (EC 2.7.1.146) (ADP-dependent
 DE Phosphofructokinase) (ADP-Pfk).
 DE PFKC OR MT1604.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanococcaceae; Methanococcoides; Methanococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

RESULT 14
 VGF-BPG4 STANDARD; PRT; 426 AA.
 ID VGF-BPG4 STANDARD; PRT; 426 AA.
 AC P03642; DT 21-JUL-1986 (Rel. 01, Created)

RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geohagen N.S.M., Weidman J.P., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Kleck H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, *Methanococcus*
 RT *jannaschii*";
 RL Science 273:1058-1073(1996).
 RN [2]
 RP CHARACTERIZATION.
 RX PubMed=1171273;
 RA Verhees C.H., Tielinga J.E., Kengen S.W.M., Stams A.J.M.,
 RA van der Oost J., de Vos W.M.;
 RT "ADP-dependent phosphofructokinases in mesophilic and thermophilic
 methanogenic archaea";
 RL J. Bacteriol. 183:7145-7153(2001).
 CC FUNCTION: Catalyzes the phosphorylation of fructose 6-phosphate to
 CC fructose 1,6-bisphosphate using ADP as the phosphate donor.
 CC -!- CATALYTIC ACTIVITY: ADP + D-fructose 6-phosphate = AMP + D-
 CC fructose 1,6-bisphosphate.
 CC -!- PATHWAY: Glycolysis, modified hyperthermophilic version.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE PFKC FAMILY OF CARBOHYDRATE KINASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 EMBL; U67600; AAB9627.1; -.
 DR TIGR; MJ1604; -.
 DR Transferase; Kinase; Glycolysis; Complete proteome.
 SQ SEQUENCE: 462 AA; 53361 MW; D91088B60DBAB104 CRC64;
 Query Match 21.0%; Score 51; DB 1; Length 462;
 Best Local Similarity 32.1%; Pred. No. 30;
 Matches 9; Conservative 6; Mismatches 13; Indels 0; Gaps 0;
 Oy 7 KMESELNFIRATTPYINYYCNPANSEK 34
 Db 338 KFKNLNVVQVHTIVVILFVCRADNPLSK 365

Search completed: March 19, 2003, 17:21:38
 Job time : 10.5 secs

GenCore version 5.1.4-p5 4578
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Om protein - protein search, using sw model

Run on: March 19, 2003, 17:18:37 ; Search time 28 seconds

(without alignments) 323.788 Million cell updates/sec

Title: US-09-674-975-1
Perfect score: 243
Sequence: I KISHLKMESLNFI RAHPTY NCEPANPSEKNSPSTQCYS 44

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SPTRMBL 21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_orcanelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rrodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	28.8	294	2 Q8RNW6	Q8rnw6 brevibacill
2	67	27.6	316	17 Q978H7	Q978H7, thermoplasm
3	61.5	25.3	580	4 Q9P2M2	Q9P2M2 homo sapien
4	61	25.1	702	10 Q9LN6	Q9ln6 arabidopsis
5	60.5	24.9	2391	5 Q27732	Q27732 Plasmidium
6	58.5	24.1	303	16 Q9CLP3	Q9CLP3 pasteurella
7	58	23.9	11	055208	055208 mus musculus
8	57	23.5	1210	10 Q8WJ8	Q8WJ8 oryza sativ
9	56.5	23.3	2425	17 Q28859	Q28859 archaeoglob
10	56	23.0	711	10 Q9SST1	Q9sst1 arabidopsis
11	55.5	22.8	299	13 Q7381	Q7381 brachydanio
12	55.5	22.8	551	5 Q25384	Q25384 hemi centrot
13	55.5	22.8	2150	5 Q44131	Q44131 caenorhabdi
14	55	22.6	149	8 Q9J74	Q9J74 caenorhabdi
15	55	22.6	380	10 Q9LQV8	Q9lqv8 arabidopsis
16	22.6	1901	10 Q9AUL6	Q9aul6 oryza sativ	

RESULT 1

Q8RNW6 PRELIMINARY; PRT; 294 AA.
ID Q8RNW6; Q8RNW6; 01-JUN-2002 (TREMBREL_21, Created)
AC Q8RNW6; DT 01-JUN-2002 (TREMBREL_21, Last sequence update)
DT 01-JUN-2002 (TREMBREL_21, Last annotation update)
DE M. Bonia.
GN BCN1MA.
OS Brevibacillus centrosporus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Paenibacillaceae; Brevibacillus.
OX NCBI_TaxID=54910;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RFLL;
RX MEDLINE=21914668; PubMed=11917015;
RA Vilkaitis G , Luuys A , Merkiene E , Timinskas A , Janulaitis A ,
RA Klimauskas S ;
RT "Circular permutation of DNA cytosine-N4 methyltransferases: in vivo
coexistence in the Bcn1 system and in vitro probing by hybrid
formation."; RT Nucleic Acids Res. 30:1547-1557(2002).
RT EMBL: AF472611; AAM03023; DR 5D7704A6FE764B73 CRC64;
RT SEQUENCE 294 AA; 34218 MW;

ALIGNMENTS

Query	Match	Length	Score	DB ID	Description
QY	2	1631	54.5	17 Q950N2	Q950n2 rhizophydiu
	1	1631	54.5	18 Q96dp2	Q96dp2 homo sapien
	1	1631	54.5	19 Q48711	Q48711 arabidopsis
	1	1631	54.5	20 Q9d211	Q9d211 mus musculus
	1	1631	54.5	21 Q9cyzo	Q9cyzo mus musculus
	1	1631	54.5	22 Q8xk9	Q8xk9 scalion vi
	1	1631	54.5	23 Q26374	Q26374 methanobact
	1	1631	54.5	24 Q59480	Q59480 pyrococcus
	1	1631	54.5	25 Q21705	Q21705 caenorhabdi
	1	1631	54.5	26 Q9FSH8	Q9fs8 lycopodium
	1	1631	54.5	27 Q9js38	Q9js38 chlamydia p
	1	1631	54.5	28 Q92707	Q92707 chlamydia p
	1	1631	54.5	29 Q87N4	Q8tn4 methanosarc
	1	1631	54.5	30 Q9ln69	Q9ln69 aranidopsis
	1	1631	54.5	31 Q9W3E3	Q9w3e3 oryza sativ
	1	1631	54.5	32 Q8w2Z7	Q8w2Z7 oryza sativ
	1	1631	54.5	33 Q9RAS3	Q9ras3 oryza sativ
	1	1631	54.5	34 Q9A1M2	Q941m2 oryza sativ
	1	1631	54.5	35 Q9S57	Q9s57 oryza sativ
	1	1631	54.5	36 Q9P16	Q9p16 oryza sativ
	1	1631	54.5	37 Q941L4	Q941l4 oryza sativ
	1	1631	54.5	38 Q9R2Z7	Q9r2Z7 oryza sativ
	1	1631	54.5	39 Q942Q4	Q942q4 oryza sativ
	1	1631	54.5	40 Q942Q8	Q942q8 oryza sativ
	1	1631	54.5	41 Q942Q9	Q942q9 oryza sativ
	1	1631	54.5	42 Q9fed6	Q9fed6 oryza sativ
	1	1631	54.5	43 Q94DC8	Q94dc8 oryza sativ
	1	1631	54.5	44 Q9W0P1	Q9w0p1 oryza sativ

DT 01-OCT-2001 (TREMBLrel. 18, Created)
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein TV1438.
 GN TV1438 OR TVG148793.
 OS Thermoplasma volcanium.
 OC Archaea; Buryarchaeota; Thermoplasma; Thermoplasmatales;
 OC Thermoplasmataceae; Thermoplasma.
 OC NCBI_TAXID=50319;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GS1 / DSM 4299 / JCM 9571;
 RX MEDLINE=20057066; PUBMED=11121031;
 RA Kawashima T., Amano N., Koike H., Higuchi S., Kawamoto T.,
 RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
 RT "Archaeal adaptation to higher temperatures revealed by genomic
 sequence of Thermoplasma volcanium.",
 RL PROC. NATL. ACAD. SCI. U.S.A. 97:14257-14262(2000).
 DR EMBL: AP00096; BAM60580.1; -
 DR InterPro: IPR01091; CNM_Mettransf.
 DR InterPro: IPR002295; D21N6_mtrrase.
 DR InterPro: IPR002941; N6/N4_Mtrase.
 DR Pfam: PF01555; N6_N4_Mtrase; 1.
 DR PRINTS: PR00506; D21N4_Mtrrase.
 DR PROSITE: PS00093; NA_Mtrase; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 316 AA; 36822 MW; 0CC2697BB8A2C863 CRC64;
 * Query Match 27.6%; Score 67; DB 17; Length 316;
 Best Local Similarity 35.9%; Pred. No. 0.3;
 Matches 14; Conservative 7; Mismatches 18; Indels 0; Gaps 0;
 OY [1]
 .Db 2 ISHFILKMEISNFIKRAHTPTVINYCEPANPSEKNSPSTQ 40
 RESULT 3
 Q9PBM2 PRELIMINARY; PRT; 580 AA.
 AC 09PBM2
 ID 09PBM2
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIAN1324 protein (fragment).
 GN KIAN1324.
 OS Homo sapiens (Human).
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC KIAN1324; EMBL: BAC037745; BAR92562.1; -.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=20018126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes.XVI.
 The complete sequences of 150 new cDNA clones from brain which code
 for large proteins in vitro.",
 RL DNA Res. 7:65-73 (2000).
 DR EMBL: BAC037745; BAR92562.1; -.
 FT NON_TER 1
 SQ SEQUENCE 580 AA; 63365 MW; 5E63C19265EC8E5C CRC64;
 * Query Match 25.3%; Score 61.5; DB 4; Length 580;
 Best Local Similarity 35.5%; Pred. No. 3.3; Matches 11; Conservative 5; Mismatches 14; Indels 1; Gaps 1;
 OY 14 IRAHTPYIINYCEPANPSEKNSPSTQCY 44
 .Db 203 LKAHQPY-GVOAUPCGPGTGNKKIKHSICYN 232
 RESULT 4
 O9LN6 PRELIMINARY; PRT; 702 AA.
 ID O9LN6
 AC O9LN6
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE F12K21.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliopsida; eudicotyledons; core eudicots; Rosidae;
 OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
 OC NCBI_TAXID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 RA Kim C., Altafi H., Bei Q., Chin C., Chiu J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A.,
 RA Toriumi M., Vaysberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC F12K21 from chromosome
 I.",
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Ecker J.R.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C.,
 RA Khan S., Kim C., Altafi H., Bei B., Chin C., Chiu J., Choi E., Conn L.,
 RA Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B.,
 RA Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N.,
 RA Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A.,
 RA Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N.,
 RA Theologis A., Ecker J.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC023219; AAH79257.1; -.
 SQ SEQUENCE 702 AA; 80578 MW; 425B0F22B76C786 CRC64;
 * Query Match 25.1%; Score 61; DB 10; Length 702;
 Best Local Similarity 35.5%; Pred. No. 4.7; Matches 11; Conservative 8; Mismatches 12; Indels 0; Gaps 0;
 OY 14 IRAHTPYIINYCEPANPSEKNSPSTQCY 44
 .Db 624 VRATTPMSNLFSCLWFNEVERFPRDQLEFA 654
 RESULT 5
 Q27732 PRELIMINARY; PRT; 2391 AA.
 ID Q27732
 AC Q27732;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Copper amine oxidase (EC 1.4.3.6).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TAXID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCQ27;
 RA Flores M.V.C.;
 RT "Molecular Biology of Pyrimidine Biosynthesis in the Human Malaria
 Parasite Plasmodium falciparum.",

DR	InterPro; PR00477; RvTase.
DR	Pfam; PR05732; Retrotans_gag; 1.
DR	Pfam; PR00658; rve; 1.
DR	Pfam; PR0078; rvt; 1.
KW	Polyprotein.
SQ	SEQUENCE 1210 AA; 133656 MW; 51687F880214E71F CRC64;
Query Match	23.5%; Score 57; DB 10; Length 1210; Best Local Similarity 23.1%; Pred. No. 30; Matches 15; Conservative 8; Mismatches 14; Indels 28; Gaps 2;
DB	1038 LKTKTENLKKRKHDSWIEELPAVLWANRTPSRATGEIPPFLLVIGAEAVLPSLTLSKSPR 1097
QY	38 SPOYC 42
Db	1098 ATWYC 1102
RESULT 9	
Q28859	PRELIMINARY; PRT; 2425 AA.
ID	028859; 01-JAN-1998 (TREMBLrel. 05', Created)
DT	01-JAN-1998 (TREMBLrel. 05', Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Surface layer protein B (SIGB-2).
GN	ATF413.
OC	Archaeoglobus fulgidus.
OC	Archaeoglobaceae; Archaeobactera; Archaeoglobales;
OC	Archaeoglobaceae; Archaeoglobus.
RN	11) NCBI_TAXID=2234;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=9809343; PubMed=939475;
RA	Klein H.-P., Dodson R.A., Tomb J.-F., White O., Nelson K.E., Retchum K.A., Dodson R.A., Gill S., Karpas N.C., Richardson D.L., Kerlavage A.R., Graham D.E., Hickey E.K., Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Cottrell M.D., Spirogs T., Artlach P., Kaine B.P., Sykes S.M., Sodjo P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith R.O., Woese C.R., Venter J.C.; "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.", Nature 390:364-370(1997); EMBL; AE00106; AAB89834.1; -.
RA	TIGR; AFL413; -.
DR	InterPro; IPK03961; FN_III.
DR	PIFM; PR0001; fn3; 1.
DR	PRINTS; PR01656; VACCYOTOXIN.
DR	SMART; SW00060; FN3; 1.
KW	Hypothetical protein; Complete proteome.
SQ	SEQUENCE 2425 AA; 266571 MW; 97E3B56843226E37 CRC64;
Query Match	23.3%; Score 56.5; DB 17; Length 2425; Best Local Similarity 30.0%; Pred. No. 73; Matches 15; Conservative 9; Mismatches 19; Indels 7; Gaps 2;
QY	1 KISHLKMKESLNTRAHPPYINN--CEPANPSE--KNPSTOYC 43
Db	1764 KISSFLKARRATERVRSISPEVEYVSNDLIEVQNQAEFLALNFGMPDYF 1813
RESULT 10	
ID	09SST1
AC	PRELIMINARY; PRT; 711 AA.
Query Match	22.8%; Score 55.5; DB 13; Length 299; Best Local Similarity 23.1%; Pred. No. 30; Matches 15; Conservative 8; Mismatches 14; Indels 28; Gaps 2;
DR	InterPro; PR00477; RvTase.
DR	Pfam; PR05732; Retrotans_gag; 1.
DR	Pfam; PR00658; rve; 1.
DR	Pfam; PR0078; rvt; 1.
KW	Polyprotein.
SQ	SEQUENCE 1210 AA; 133656 MW; 51687F880214E71F CRC64;
Query Match	23.5%; Score 57; DB 10; Length 1210; Best Local Similarity 23.1%; Pred. No. 30; Matches 15; Conservative 8; Mismatches 14; Indels 28; Gaps 2;
DB	1038 LKTKTENLKKRKHDSWIEELPAVLWANRTPSRATGEIPPFLLVIGAEAVLPSLTLSKSPR 1097
QY	38 SPOYC 42
Db	1098 ATWYC 1102
RESULT 9	
Q28859	PRELIMINARY; PRT; 2425 AA.
ID	028859; 01-JAN-1998 (TREMBLrel. 05', Created)
DT	01-JAN-1998 (TREMBLrel. 05', Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Surface layer protein B (SIGB-2).
GN	ATF413.
OC	Archaeoglobus fulgidus.
OC	Archaeoglobaceae; Archaeobactera; Archaeoglobales;
OC	Archaeoglobaceae; Archaeoglobus.
RN	11) NCBI_TAXID=2234;
RP	SEQUENCE FROM N.A.
RA	Spiegel L.A., Huang E.N., Nascimento L.U., de la Bastide M., Vil D.M., Preston R.R., Matero A., Shah R., O'shaughnessy A., Rodriguez M., Shekter M., Schutz K., See L.H., Swaby I., Habermann K., Dediha N.N., Mewes H.W., Lemcke K., Mayer K.F.X.; Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
RA	EMBL; AL16831; CAB82130.1; -.
DR	EMBL; AL168315; CAB78086.1; -.
KW	Hypothetical protein.
SQ	SEQUENCE 711 AA; 81270 MW; E49BBE6FD92AFF5A CRC64;
Query Match	23.0%; Score 56; DB 10; Length 711; Best Local Similarity 32.3%; Pred. No. 24; Matches 10; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
DB	632 VREHTPMNLSCWLWNEVERTPRDQLSFA 662
RESULT 11	
QY	14 IRAHTPYINNYCEPANPSEKNSSPSTOYCYS 44
ID	073781
AC	073781; 01-AUG-1998 (TREMBLrel. 07, Created)
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT	01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE	Fork head domain protein FKD5.
GN	FKD5.
OS	Brachydanio rerio (Zebrafish)
OC	Eukaryota; Metazoa; Chordata; Ciliata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
OC	NCBI_TAXID=7955;
RN	11) NCBI_TAXID=7955;
RP	SEQUENCE FROM N.A.
RX	MEDLINE=98350246; PubMed=9683740;
RA	Odenthal J., Nusslein-Volhard C.; "Fork head domain genes in zebrafish.", Dev. Genes Evol. 208:245-258(1998).
RT	EMBL; AF05248; AAC06365.1; -.
RL	HSSP; Q63245; 2HFF.
DR	ZFIN; ZDB-GENE-990415-77; foxb1.1.
DR	InterPro; IPR01766; TF_Fork_head.
DR	Pfam; PR0250; Fork_head; 1.
DR	PRINTS; PR0053; FORKHEAD.
DR	ProDom; P000425; TF_Fork_head; 1.
DR	SMART; SW00039; FH; 1.
DR	PROSITE; PR00657; FORK_HEAD_1.
DR	PROSITE; PR00658; FORK_HEAD_2; UNKNOWN_1.
DR	PROSITE; PR00659; FORK_HEAD_3; 1.
SQ	SEQUENCE 299 AA; 33219 MW; A2C731F218EA9EEA CRC64;

RESULT	14	PRELIMINARY;	PRT;	149 AA.
ID	Q9TJ4			
AC	Q9TJ4			
DT	01-MAY-2000	(TREMBLrel. 13, Created)		
DT	01-MAY-2000	(TREMBLrel. 13, Last sequence update)		
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
DE	RNA polymerase (Fragment).			
OS	Chloroplast.			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Gnetophyta; Gnetopsida; Gnetales; Gnetae; Gnetaum.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=9946856; Pubmed=10473771;			
RA	Samigullin T., Martin W., Troitsky A., Antonov A.;			
RT	"Molecular data from the chloroplast rpoC1 gene suggest a deep and distinct dichotomy of contemporary spermatophytes into two monophylums: gymnosperms (including Gnetales) and angiosperms. ";			
RA	J. Mol. Evol. 49:315-319 (1999).			
DR	EMBL: A012667; CAB56787.1; -			
DR	Intelpub: IRO0022; RNA_POLA.			
DR	PFam: PF00623; RNA_POLA; 1.			
KW	Chloroplast.			
FT	NON-TER 1			
FT	NON-TER 149 AA; 17137 MW; 09103F3C78D4DE52 CRC64;			
SQ	SEQUENCE 149 AA;			
Query Match	22.6%	Score 55;	DB 10;	Length 380;
Best Local Similarity	34.8%	Pred. No. 6.7;	Length 149;	
Matches	8	Conservative	6	Mismatches 9; Indels 0; Gaps 0;
Qy	21 INYNC PANPBEKNSSTQCY 43			
Db	55 ISQFRCRPSNPTRKKFLPBEVNLCF 77			
RESULT	15			
ID	Q9LQV8	PRELIMINARY;	PRT;	380 AA.
AC	Q9LQV8:			
DT	01-OCT-2000	(TREMBLrel. 15, Created)		
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	F10B6.13.			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae;			
OC	eurosidios II; Brassicales; Brassicaceae; Arabidopsis.			
OX	NCBI_TAXID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Chao Q., Shinn P., Dunn P., Buehler E., Kahn S., Kim C., Walker M., Williams S., Altafai H., Araujo R., Conn L., Conway A.B., Gonzalez A., Hansen N.F., Huizar L., Kramenetskaia I., Lenz C., Li J., Liu S., Luos S., Rowley D., Schwartz J., Toriumi M., Vysotskaya V., Yu G., Davis R.W., Federspiel N.A., Theologis A., Ecker J.R.,			
RT	"Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome 1. ";			
RT	Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	Ecker J.R.;			
RA	Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Ecker J.R.;			
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.			
RN	[4]			